

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 05:55:10 ; Search time 6823 Seconds  
(without alignments)  
6753.761 Million cell updates/sec

Title: US-09-403-882a-1

Sequence: 1 atggccgaggtcagctgcga.....ggcagaagaagcagcttag 951

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Genembl: \*  
1: gb\_ba: \*  
2: gb\_hcg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sbs: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	749.6	78.8	1256	6	AR175770 Sequence
2	749.6	78.8	1256	6	AR232005 Sequence
3	749.6	78.8	1256	6	AX136010 Sequence
4	749.6	78.8	1256	6	AX136779 Sequence
5	749.6	78.8	1256	6	AX137830 Sequence
6	749.6	78.8	1256	6	BD000153 Proceess f
7	749.6	78.8	1256	6	BD010885 Proceess f
8	737	77.5	843	6	AX781447 Sequence
9	737	77.5	843	6	AX795414 Sequence
10	699.4	73.5	726	6	AX353652 Sequence
11	655.4	68.9	738	6	A41674 Sequence 1
12	651	68.5	711	6	A25748 Variable re
13	651	68.5	711	6	AR051416 Sequence re
14	580.6	61.1	672	6	A25746 Variable re
15	580.6	61.1	672	6	AR051415 Sequence
16	548	57.6	1725	6	AX001509 Sequence
17	543.6	57.2	793	6	A41676 Sequence 3
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#### ALIGNMENTS

RESULT 1	AR175770	1256 bp	DNA	linear	PAT 17-DEC-2001
LOCUS	AR175770				
DEFINITION	Sequence 7 from patent US 6309861.				
ACCESSION	AR175770				
VERSION	AR175770.1	GI:17917069			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1256)				
AUTHORS	Ambrosius,D., Rudolph,R., Schaeffner,J. and Schwarz,E.				
TITLE	Process for the production of naturally folded and secreted proteins				
JOURNAL	Patent: US 6309861-A 7 30-OCT-2001;				
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#### ORIGIN

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Best Local Similarity	98.2%	Pred. No. 3e-189;		
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DB	199	ATGGCCGAGGTCAAGCTGCAAGTCTGGGGGAGGCTTAGTGGAGGAGGTC	258	
QY	61	AAACTCTCCTGTCACAGCTCTGATTCACTTTCAGTAGCTTTGGAATGCACTGGTTCT	120	
DB	259	AAACTCTCCTGTCACAGCTCTGATTCACTTTCAGTAGCTTTGGAATGCACTGGTTCT	318	
QY	121	CAGGCTTCAGAGAGGGCTGAGTGGCTGCATATATTATGTTGGCACTAGTACATC	180	
DB	319	CAGGCTTCAGAGAGGGCTGAGTGGCTGCATATATTATGTTGGCACTAGTACATC	378	
QY	181	TACTATGACAGACAGAGGAGGAGGAGTTCACCATCTCCAGAGCAATCCAGAACACC	240	
DB	379	TACTATGACAGACAGAGGAGGAGGAGTTCACCATCTCCAGAGCAATCCAGAACACC	438	
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Db 619 ATCATGTCTGCATCTCCAGGGGAGAGGGTCAACATGACCTGAGAGCCGATTCAAGTGA 678
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Db 679 AGGTACATGAACTGGTTCCAGAGAGTCAAGGACACTCCCAAAAGATGATTTATGAC 738
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LOCUS AR232005
DEFINITION Sequence 7 from patent US 6455279.
ACCESSION AR232005
VERSION AR232005.1 GI:27273847
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1256)
AUTHORS Ambrosius D., Rudolph R., Schaeffner J. and Schwarz E.
TITLE Process for the production of naturally folded and secreted
JOURNAL proteins by co-secretion of molecular chaperones
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 78.8%; Score 749.6; DB 6; Length 1256;
Best Local Similarity 98.2%; Pred. No. 3e-189;
Matches 758; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
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Qy 721 GCAGAACAAAATCTCATCTCAGAGAGAGATCTGAATGGGGCGCTGCAGCAAC 772
Db 919 GCAGAACAAAATCTCATCTCAGAGAGAGATCTGAATGGGGCGCGCATAGTAAC 970

RESULT 3
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LOCUS AX136010
DEFINITION Sequence 7 from Patent EP1054063.
ACCESSION AX136010
VERSION AX136010.1 GI:14272438
KEYWORDS
SOURCE Escherichia coli.
ORGANISM Escherichia coli.
REFERENCE 1
AUTHORS Ambrosius D., Rudolph R., Schaeffner J. and Schwarz E.
TITLE Process for the production of naturally folded and secreted
JOURNAL proteins
FEATURES
source Location/Qualifiers
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QY 721 GCAGAACAAAATCATCTCAGAGAGATGTAATGGGGCCGTCGACGAC 772  
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LOCUS AX137830 1256 bp DNA linear PAT 30-MAY-2001  
DEFINITION Sequence 7 from Patent EP1077262.  
ACCESSION AX137830  
VERSION AX137830.1 GI:14273986  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
F. HOFMANN-LA ROCHE AG (CH)  
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Query Match 78.8%; Score 749.6; DB 6; Length 1256;  
Best Local Similarity 98.2%; Pred. No. 3e-189;  
Matches 758; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGCCGAGGTCAGCTCAGAGAGTCAAGGGAGGCTTAGTCAGCCTCGAGGTCGCCG 60  
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QY 61 AAATCTCTCTGTGAGCCTCTGGAATTCAGTTAGCTTTGGAATGCACTGGGTTGCT 120  
DB 259 AAATCTCTCTGTGAGCCTCTGGAATTCAGTTAGCTTTGGAATGCACTGGGTTGCT 318

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QY 181 TACTATGAGACACAGTGAAGGAGCATTCACCATCTCCAGAGACATCCCAAGAACACC 240  
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QY 241 CTGTTCTCTGCAATGACAGTCTTAAGGTCTGAGACACGGTATATTAATCTGTGCAAGA 300  
DB 439 CTGTTCTCTGCAATGACAGTCTTAAGGTCTGAGACACGGCATATTAATCTGTGCAAGA 498

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DB 919 GCAGAACAAAATCATCTCAGAGAGATCTGAAATGGGGCCGTCAGTAAC 970

RESULT 6  
BD000153 1256 bp DNA linear PAT 31-JAN-2002  
LOCUS BD000153  
DEFINITION Process for producing protein that is spontaneously folded and secreted.  
ACCESSION BD000153.1 GI:18623232  
VERSION BD000153.1 JP 2000316591-A/4.  
KEYWORDS unclassified  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 1256)  
AUTHORS Ambrosius, D., Ludlf, R., Syefuna, J. and Schwarz, E.  
TITLE Process for producing protein that is spontaneously folded and Patent: JP 2000316591-A 4 21-NOV-2000;  
JOURNAL F. HOFMANN LA ROCHE AG  
COMMENT OS E. coli  
PN 21-NOV-2000  
PD 21-NOV-2000  
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PR 26-APR-1999 EP 99107412.1  
PI DOROTE AMBROSIOUS, RINER LUDLF, JERUG SYEFUNA, ELIZABETH SCHWARZ  
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Query Match 78.8%; Score 749.6; DB 6; Length 1256;  
Best Local Similarity 98.2%; Pred. No. 3e-189;  
Matches 758; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGCCGAGGTCAGCTCAGAGAGTCAAGGGAGGCTTAGTCAGCCTCGAGAGTCCCGG 60  
DB 199 ATGCCGAGGTCAGCTCAGAGAGTCTGGGGAGGCTTAGTCAGCCTCGAGAGTCCCGG 258

QY 61 AAATCTCTCTGTGAGCCTCTGGAATTCAGTTAGCTTTGGAATGCACTGGGTTGCT 120  
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QY 121 CAGGCTCAGAGAGAGGGCTGGAGTGGGTCGATATATTAGTAGGGCAGTAGTACCATC 180  
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RESULT 7				
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LOCUS				
DEFINITION			Process for producing spontaneously folded secreted protein by co-secretion of molecular Chaperone.	
ACCESSION			BD010885	
VERSION			BD010885.1 GI:18639258	
KEYWORDS			JP 2001061487-A/4.	
SOURCE			Escherichia coli	
ORGANISM			Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.	
REFERENCE			1 (bases 1 to 1256)	
AUTHORS			Ambrosius,D., Ludlf,R., Schaffner,J. and Schwarz,B.	
TITLE			Process for producing spontaneously folded secreted protein by co-secretion of molecular Chaperone	
JOURNAL			Patent: JP 2001061487-A 4 13-MAR-2001;	
COMMENT			F HOFMANN LA ROCHE AG OS Escherichia coli PN JP 2001061487-A/4 PD 13-MAR-2001 PF 31-JUL-2000 JP 2000231804 PR 29-JUL-1999 EP 9914811.5 PI DOROCY AMBROSIOUS,RIMER LUDLF,JAEK SCHAFFNER,ELIZABETH SCHWARZ PC C12N15/09,C12N9/48,C12P21/02,C12P21/02,C12P21/08/C12N1/21, PC (C12N9/48,C12R1:19),(C12P21/02,C12R1:19),(C12P21/08,C12R1:19), PC C12N15/00	
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	Best Local Similarity	98.2%; Pred. No. 3e-189;	
	Matches 758; Conservative	0; Mismatches 14; Indels 0; Gaps 0.	
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Qy	61 AAATCTCTCTGTGACGCTCTGGAATTCACTTTCACTAGTACCTTTGGAAATGCACTGGGTTCTG	120	
Db	259 AAATCTCTCTGTGACGCTCTGGAATTCACTTTCACTAGTACCTTTGGAAATGCACTGGGTTCTG	318	
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Db	739 ACATCCAAACGTGTTCTGAGAGTCCCTGCTGCTTCACTGAGGACATGGGCTGGGACCTCT	798	
Qy	601 TACTCTCTCACAATCAGACAGATGAGAGCTGGAAGATCTGCACTTACTATGTCACAGAG	660	
Db	799 TACTCTCTCACAATCAGACAGATGAGAGCTGGAAGATCTGCACTTACTATGTCACAGAG	858	
Qy	661 TGAGTGTGTAAACCACTCAAGTTCGGTGTGGTCTGGGACCAAGCTGAGCTGAAACGGGCGGCC	720	
Db	859 TGAGTGTGTAAACCACTCAAGTTCGGTGTGGTCTGGGACCAAGCTGAGCTGAAACGGGCGGCC	918	
Qy	721 GCAGAAACAAAAATCATCTCAGAGAGAGATCTGAATGGGGCCGTCGAGCAAC	772	
Db	919 GCAGAAACAAAAATCATCTCAGAGAGAGATCTGAATGGGGCCGTCAGTATGTTAAC	970	
RESULT 8			
AX781447		843 bp	DNA linear PAT 17-JUL-2003
LOCUS	AX781447		
DEFINITION	Sequence 3 from Patent EP1321524.		
ACCESSION	AX781447		
VERSION	AX781447.1 GI:32949302		
KEYWORDS			
SOURCE			
ORGANISM			
	synthetic construct		
	synthetic construct		
	other sequences; artificial sequences.		

REFERENCE 1  
AUTHORS Mahn, A., Hantke, S. and Petesch, D.  
TITLE Method of increasing the transgene-coded biomolecule content in  
JOURNAL Organisms  
Patent: EP 1321524-A 3 25-JUN-2003;  
Duering, Klaus, Dr. (DE)  
FEATURES Location/Qualifiers  
source 1..843  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of the Artificial Sequence:  
scFv-antibody"

ORIGIN  
Query Match 77.5%; Score 737; DB 6; Length 843;  
Best Local Similarity 97.4%; Pred. No. 7.1e-186;  
Matches 749; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 4 GCCGAGTCAAGCTGACAGAGTCAGGGGAGGCTTAGTACAGCTGAGAGGTCGCCGAAA 63  
DB 70 GCTGATGTGACAGCTGAGTGTGAGTGTGAGGAGGCTTAGTACAGCTGAGAGGTCGCCGAAA 129  
QY 64 CTCTCTGTGACAGCTCTGATTTCACTTTCAGTAGCTTGAATGACATGGGTTGGTCAG 123  
DB 130 CTCTCTGTGACAGCTCTGATTTCACTTTCAGTAGCTTGAATGACATGGGTTGGTCAG 189  
QY 124 GCTCAGAGAGAGGGCTGAGTGGGTGCGATATATTAGTAGGAGTAGTACATCTAC 183  
DB 190 GCTCAGAGAGAGGGCTGAGTGGGTGCGATATATTAGTAGGAGTAGTACATCTAC 249  
QY 184 TATGACAGACAGTAGAAGGAGAGATTCACATCTCCAGAGACAAATCCCAAGAACCCCTG 243  
DB 250 TATGACAGACAGTAGAAGGAGAGATTCACATCTCCAGAGACAAATCCCAAGAACCCCTG 309  
QY 244 TTCTGTCAAAATACAGATCTAAGTCTGAGGACACGGTATGATTTACTGTCAAGAGAT 303  
DB 310 TTCTGTCAAAATACAGATCTAAGTCTGAGGACACGGTATGATTTACTGTCAAGAGAT 369  
QY 304 TACGGGGCTTATTGGGGCCAAAGGACACAGGTACCGTCTCTCAGTGGAGGCGGCTCA 363  
DB 370 TACGGGGCTTATTGGGGCCAAAGGACACAGGTACCGTCTCTCAGTGGAGGCGGCTCA 429  
QY 364 GGGGAGGTGGCTCTGCGGTGGCGGATGAGACATTGAGACTACCCAGTCTCCAGCAATC 423  
DB 430 GGGGAGGTGGCTCTGCGGTGGCGGATGAGACATTGAGACTACCCAGTCTCCAGCAATC 489  
QY 424 ATGTCTGATCTCCAGGGGAGAGGTCACATGACCTGAGTCCAGTTCAAGTGAAG 483  
DB 490 ATGTCTGATCTCCAGGGGAGAGGTCACATGACCTGAGTCCAGTTCAAGTGAAG 549  
QY 484 TACATGAACCTGGTTCACACAGAGTCAAGGACCTCCCAAAAGATGATTTATGACACA 543  
DB 550 TACATGAACCTGGTTCACACAGAGTCAAGGACCTCCCAAAAGATGATTTATGACACA 609  
QY 544 TCCAAACTGTCTTCTGAGAGTCCCTGTCTGCTTCAAGTGGAGTGGGCTCTTTAC 603  
DB 610 TCCAAACTGTCTTCTGAGAGTCCCTGTCTGCTTCAAGTGGAGTGGGCTCTTTAC 669  
QY 604 TCTCTCACAATCAGAGAGTGAAGTGCCTTACTTACTACTGAGCAGAGTGG 663  
DB 670 TCTCTCACAATCAGAGAGTGAAGTGCCTTACTTACTACTGAGCAGAGTGG 729  
QY 664 AGTAGTAACCACTACAGTTCGGTCTGAGGACCAAGCTGAGACTGAAACGGGCGGCGCA 723  
DB 730 AGTAGTAACCACTACAGTTCGGTCTGAGGACCAAGCTGAGACTGAAACGGGCGGCGCA 789  
QY 724 GAACAAAAAATCTATCTCAGAAAGAGATCTGAATGGGCGGCTGAGGAAC 772  
DB 790 GAACAAAAAATCTATCTCAGAAAGAGATCTGAATGGATTCAAAGACGAAC 838

AX795414  
LOCUS AX795414 843 bp DNA linear PAT 04-OCT-2003  
DEFINITION Sequence 3 from Patent WO03052109.  
ACCESSION AX795414  
VERSION AX795414.1 GI:37516087  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Duering, K., Mahn, A., Hantke, S. and Petesch, D.  
TITLE Method of increasing the transgene-coded biomolecule content in  
JOURNAL Organisms  
Patent: WO 03052109-A 3 26-JUN-2003;  
Duering, Klaus (DE)  
FEATURES Location/Qualifiers  
source 1..843  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="scFv-antibody"

ORIGIN  
Query Match 77.5%; Score 737; DB 6; Length 843;  
Best Local Similarity 97.4%; Pred. No. 7.1e-186;  
Matches 749; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 4 GCCGAGTCAAGCTGACAGAGTCAGGGGAGGCTTAGTACAGCTGAGAGGTCGCCGAAA 63  
DB 70 GCTGATGTGACAGCTGAGTGTGAGTGTGAGGAGGCTTAGTACAGCTGAGAGGTCGCCGAAA 129  
QY 64 CTCTCTGTGACAGCTCTGATTTCACTTTCAGTAGCTTGAATGACATGGGTTGGTCAG 123  
DB 130 CTCTCTGTGACAGCTCTGATTTCACTTTCAGTAGCTTGAATGACATGGGTTGGTCAG 189  
QY 124 GCTCAGAGAGAGGGCTGAGTGGGTGCGATATATTAGTAGGAGTAGTACATCTAC 183  
DB 190 GCTCAGAGAGAGGGCTGAGTGGGTGCGATATATTAGTAGGAGTAGTACATCTAC 249  
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QY 244 TTCTGTCAAAATACAGATCTAAGTCTGAGGACACGGTATGATTTACTGTCAAGAGAT 303  
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DB 370 TACGGGGCTTATTGGGGCCAAAGGACACAGGTACCGTCTCTCAGTGGAGGCGGCTCA 429  
QY 364 GGGGAGGTGGCTCTGCGGTGGCGGATGAGACATTGAGACTACCCAGTCTCCAGCAATC 423  
DB 430 GGGGAGGTGGCTCTGCGGTGGCGGATGAGACATTGAGACTACCCAGTCTCCAGCAATC 489  
QY 424 ATGTCTGATCTCCAGGGGAGAGGTCACATGACCTGAGTCCAGTTCAAGTGAAG 483  
DB 490 ATGTCTGATCTCCAGGGGAGAGGTCACATGACCTGAGTCCAGTTCAAGTGAAG 549  
QY 484 TACATGAACCTGGTTCACACAGAGTCAAGGACCTCCCAAAAGATGATTTATGACACA 543  
DB 550 TACATGAACCTGGTTCACACAGAGTCAAGGACCTCCCAAAAGATGATTTATGACACA 609  
QY 544 TCCAAACTGTCTTCTGAGAGTCCCTGTCTGCTTCAAGTGGAGTGGGCTCTTTAC 603  
DB 610 TCCAAACTGTCTTCTGAGAGTCCCTGTCTGCTTCAAGTGGAGTGGGCTCTTTAC 669  
QY 604 TCTCTCACAATCAGAGAGTGAAGTGCCTTACTTACTACTGAGCAGAGTGG 663  
DB 670 TCTCTCACAATCAGAGAGTGAAGTGCCTTACTTACTACTGAGCAGAGTGG 729  
QY 664 AGTAGTAACCACTACAGTTCGGTCTGAGGACCAAGCTGAGACTGAAACGGGCGGCGCA 723



Db 730 AGTAGTAATCCACTCTTCCTGGTGTCTGGAGCCAGACTGAGAGCTGAACGGGCGGCGCA 789

Qy 724 GAACAAAATCATCTCAGAGAGATCTGAATGGGCGCTGACGCAAC 772

Db 790 GAACAAAATCATCTCAGAGAGATCTGAATGGATTCGAAGACGAC 838

RESULT 10

AX353652 726 bp DNA linear PAT 06-FEB-2002

LOCUS Sequence 1 from Patent WO0204020.

DEFINITION AX353652

ACCESSION AX353652

VERSION AX353652.1 GI:18618722

KEYWORDS

SOURCE synthetic construct

ORGANISM other sequences; artificial sequences.

REFERENCE 1

AUTHORS Duerling, K. and Brinkmann, O.

TITLE Pathogen resistance in organisms

JOURNAL Patent: WO 0204020-A 1 17-JAN-2002;

MPB Cologne GmbH (DE)

FEATURES

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1. .726

/organism="synthetic construct"

/mol\_type="unassigned DNA"

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/note="Beschreibung der kuenstlichen Sequenz: beFV-Antikuerper, der 2-Phenylloxazol-5-on Bindet"

ORIGIN

Query Match 73.5%; Score 699.4; DB 6; Length 726;

Best Local Similarity 97.8%; Pred. No. 8e-176;

Matches 709; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 1 ATGGCCGAGCTCAAGCTGACAGAGTCAAGGGGAGGCTTACTGACCTGAGGGGTCCTCCG 60

Db 1 ATGGCTGATGTGACAGCTGAGTCTGGGGGAGGCTTACTGACCTGAGGGGTCCTCCG 60

Qy 61 AAACCTCTCTGTGACACCTCTGTGATTCACCTTACAGTACCTTGGATGACCTGGTTCC 120

Db 61 AAACCTCTCTGTGACACCTCTGTGATTCACCTTACAGTACCTTGGATGACCTGGTTCC 120

Qy 121 CAGGCTCCAGAGAGGGGCTGAGTGGGTGCGATATTTAGTAGTGAGAGTATCCATATC 180

Db 121 CAGGCTCCAGAGAGGGGCTGAGTGGGTGCGATATTTAGTAGTGAGAGTATCCATATC 180

Qy 181 TACTATGACAGACAGTGAAGGAGCATTCACCATCTCCAGAGACATCCCAAGAACCC 240

Db 181 TACTATGACAGACAGTGAAGGAGCATTCACCATCTCCAGAGACATCCCAAGAACCC 240

Qy 241 CTGTCTCTGCAATGACCACTTAAGTCTGAGAGACAGGCTATGTTTACTGTGCAAG 300

Db 241 CTGTCTCTGCAATGACCACTTAAGTCTGAGAGACAGGCTATGTTTACTGTGCAAG 300

Qy 301 GATTACGGGGCTTAATGGGGCCAAAGGACCAAGGTACCGCTCTCCAGGTGAGGGGCG 360

Db 301 GATTACGGGGCTTAATGGGGCCAAAGGACCAAGGTACCGCTCTCCAGGTGAGGGGCG 360

Qy 361 TCAGGGCGAGGTGCTGTGGCGGTGGCGGATTCGACATTGAGTCAACCAAGTCTCCAGCA 420

Db 361 TCAGGGCGAGGTGCTGTGGCGGTGGCGGATTCGACATTGAGTCAACCAAGTCTCCAGCA 420

Qy 421 ATCATGTCTGCAATCTCCAGGGGAGAGGGTCAACATGACCTGAGTGCAGATTCAAGTGA 480

Db 421 ATCATGTCTGCAATCTCCAGGGGAGAGGGTCAACATGACCTGAGTGCAGATTCAAGTGA 480

Qy 481 AGGTACATGAATCGTTCCAAAGAGTCAAGGACCTCCCAAAAGATGATTTATGAC 540

Db 481 AGGTACATGAATCGTTCCAAAGAGTCAAGGACCTCCCAAAAGATGATTTATGAC 540

Qy 541 ACATCCAAATGCTCTTCTGGAGTCCCTGCTCGCTTCAAGTGGAGTGGGTCTGGGACCTCT 600

Db 541 ACATCCAAATGCTCTTCTGGAGTCCCTGCTCGCTTCAAGTGGAGTGGGTCTGGGACCTCT 600

Db 541 ACATCCAAATGCTCTTCTGGAGTCCCTGCTCGCTTCAAGTGGAGTGGGTCTGGGACCTCT 600

Qy 601 TACTCTCTCAATCAGACAGATGAGAGTGAAGATGCTGCCACTTACTACTGCGACAG 660

Db 601 TACTCTCTCAATCAGACAGATGAGAGTGAAGATGCTGCCACTTACTACTGCGACAG 660

Qy 661 TGGAGTAGTAACCCACTCAAGTTGGTGTGGAGCCAGACTGGAGCTGAACGGGCGGCC 720

Db 661 TGGAGTAGTAATCCACTCACTTGGTGTGGAGCCAGACTGGAGCTGAACGGGCGGCC 720

Qy 721 GCAGA 725

Db 721 GCATA 725

RESULT 11

A41674 738 bp DNA linear PAT 05-MAR-1997

LOCUS Sequence 1 from Patent EP0630968.

DEFINITION A41674

ACCESSION A41674

VERSION A41674.1 GI:2297297

KEYWORDS

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 738)

AUTHORS Fritz, H., Hennecke, F. and Kolmar, H.

TITLE Genetic selection of proteins able to bind a ligand by signal-transduction in a microorganism

JOURNAL Patent: EP 0630968-A 1 28-DEC-1994;

BEHRINGWERKE AG (DE)

COMMENT Other publication JP 6343472 941220

Other publication AU 6461494 941215

Other publication CA 2125536 941211

Other publication DE 4319296 941215.

FEATURES

source

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/organism="unidentified"

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/db\_xref="taxon:32644"

1. .720

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/protein\_id="CAA02622.1"

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CDS

ORIGIN

Query Match 68.9%; Score 655.4; DB 6; Length 738;

Best Local Similarity 95.0%; Pred. No. 4.7e-164;

Matches 677; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 2 TGGCCAGAGTCAAGCTGACAGAGTCAAGGGGAGGCTTAAGTGCAGCCTTGAGAGGTCCCGGA 61

Db 8 TCACCTACAGTACAGCTGAGTGAAGCTTGGGGAGGCTTTGTGACGCTGAGAGGTTCCCGGA 67

Qy 62 AACTCTCTGTGAGAGCTCTGATTCACCTTCAAGTCTTGAATGCACTGGGTTGCTC 121

Db 62 AACTCTCTGTGAGAGCTCTGATTCACCTTCAAGTCTTGAATGCACTGGGTTGCTC 127

Qy 68 AACTCTCTGTGAGAGCTCTGATTCACCTTCAAGTCTTGAATGCACTGGGTTGCTC 127

Db 122 AGGCTCCAGAGAGGGGCTGAGTGGGTGCGATATTAAGTATGSCAGTAGTACATCT 181

Qy 128 AGGCTCCAGAGAGGGGCTGAGTGGGTGCGATATTAAGTATGSCAGTAGTACATCT 187

Db 182 ACTATGACAGACAGAGGAGGAGTTCACCATCTCCAGAGACATCCCAAGAACACC 241

Qy 188 ACTATGACAGACAGAGGAGGAGTTCACCATCTCCAGAGACATCCCAAGAACACC 247

Db 188 ACTATGACAGACAGAGGAGGAGTTCACCATCTCCAGAGACATCCCAAGAACACC 247

QY 242 TGTCTCTGCAATGACCACTTAAGTCTGAGAGACCGTCACTGTTTACTGTGCAAG 301  
Db 248 TGTCTCTGAGATGACCACTTAAGTCTGAGAGACCGTCACTGTTTACTGTGCAAG 307  
QY 302 ATTACGGGGCTTAATGAGGGGCAAGGGACCAAGGTCAAGGTCTCCAGGTGAGGGGCT 361  
Db 308 ATTACGGGGCTTAATGAGGGGCAAGGGACCAAGGTCTCCAGGTGAGGGGCT 367  
QY 362 CAGGCGAGAGTGGCTCTGGCGGTGGCGGATCGGAACATTGAGCTCAACCAAGTCTCCAGCAA 421  
Db 368 CAGGCGAGAGTGGCTCTGGCGGTGGCGGATCGGAACATTGAGCTCTCCAGCAA 427  
QY 422 TCATGTCTGCATCTCCAGGGGAGAGGGTACCATGACCTGACAGTGCAGTTCAAGTTAA 481  
Db 428 TCATGTCTGCATCTCCAGGGGAGAGGGTACCATGACCTGACAGTGCAGTTCAAGTTAA 487  
QY 482 GGTACATGAATGTTTCCAAAGAGTCAAGGACCTCCCAAAAGATGGAATTTATGACA 541  
Db 488 GGTACATGAATGTTTCCAAAGAGTCAAGGACCTCCCAAAAGATGGAATTTATGACA 547  
QY 542 CATCCAACTGTCTTCTGAGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTT 601  
Db 548 CATCCAACTGTCTTCTGAGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTT 607  
QY 602 ACTCTCTCAGATCAAGAGATGAGAGGCTGAAGATGCTGCCCTTAATCTGCTCCAGCAGT 661  
Db 608 ACTCTCTCAGATCAAGAGATGAGAGGCTGAAGATGCTGCCCTTAATCTGCTCCAGCAGT 667  
QY 662 GGAGTAGTAACCACTCAAGTTCGGTGTGGGAGCCAAAGCTGGAGCTGAAACGG 714  
Db 668 GGAGTAGTAACCACTCAAGTTCGGTGTGGGAGCCAAAGCTGAAACGG 720

RESULT 12  
LOCUS A25748 711 bp DNA linear PAT 14-MAR-1995  
DEFINITION Variable region heavy and kappa light chain linked genes (stage 3).  
ACCESSION A25748  
VERSION A25748.1 GI:904741  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 711)  
AUTHORS  
TREATMENT OF CELL POPULATIONS  
JOURNAL Patent: WO 9303151-A 59 18-FEB-1993;  
FEATURES  
source location/Qualifiers  
1..711  
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/db\_xref="taxon:32630"  
/note="NO10/12.5-stage 2"  
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V\_region /product="variable region of Ig heavy chain"  
misc\_feature 346..387  
/note="linker peptide"  
V\_region 388..711  
/product="variable region of Ig kappa light chain"  
ORIGIN

Query Match 68.5%; Score 651; DB 6; Length 711;  
Best Local Similarity 95.0%; Pred. No. 7.1e-163;  
Matches 672; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
QY 7 GAGGTCAAGCTCAGAGAGTCAAGGAGGCTTAAGTCAAGGCTCGAGGGTCCCGGAAACTC 66  
Db 1 GATGTGCAAGCTGTGAGAGTCTGGGGAGGCTTAAGTCAAGGCTCGAGGGTCCCGGAAACTC 60  
QY 67 TCCTGTGAGCCTCTGAGATTCATTTCAAGTACCTTTGGAATGCACTGGGTTGTCAGAGCT 126  
Db 61 TCCTGTGAGCCTCTGAGATTCATTTCAAGTACCTTTGGAATGCACTGGGTTGTCAGAGCT 120

QY 127 CCAGGAAGGGGCTGAGTGGGTGCGCATATATTTAGTAGTGCGAGTAGTACCTTACTAT 186  
Db 121 CCAGGAAGGGGCTGAGTGGGTGCGCATATATTTAGTAGTGCGAGTAGTACCTTACTAT 180  
QY 187 GCAGCAAGTAGGAAGGGGAGATTCACCATCTCCAGAGACATATCCCAAGAACCCCTGTTT 246  
Db 181 GCAGCAAGTAGGAAGGGGAGATTCACCATCTCCAGAGACATATCCCAAGAACCCCTGTTT 240  
QY 247 CTGCAATGACCAAGTCTAAGTCTGAGAGACAGGTCAATGATTTACTGTGCAAGATTAAC 306  
Db 241 CTGCAATGACCAAGTCTAAGTCTGAGAGACAGGTCAATGATTTACTGTGCAAGATTAAC 300  
QY 307 GGGGCTTATTTGGGGGCAAGGGACCAAGGTCAAGCTCTCTTCAAGTGGAGGGGCTCAGGC 366  
Db 301 GGGGCTTATTTGGGGGCAAGGGACCTCTGCTCACTGTCTTGCAGGGGTGTGTGCGGT 360  
QY 367 GGAGGTGCTCTGGGCGGTGGGGAGATCGGACATTTGAGTCAACCATCTCCAGCAATTCATG 426  
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QY 427 TCTGATCTCCAGGGGAGAGGGTCAACATGACCTGACAGTGCAGTTCAAGTGAAGTAC 486  
Db 421 TCTGATCTCCAGGGGAGAGGGTCAACATGACCTGACAGTGCAGTTCAAGTGAAGTAC 480  
QY 487 ATGAAGTGGTTCACAGAAAGTCAAGGACCTCCCAAAAGATGGAATTTATGACATTC 546  
Db 481 ATGAAGTGGTTCACAGAAAGTCAAGGACCTCCCAAAAGATGGAATTTATGACATTC 540  
QY 547 AAACGTCTTCTGAGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTTACTCT 606  
Db 541 AAACGTCTTCTGAGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTTACTCT 600  
QY 607 CTCACAAATCAGCAGATGAGGCTGAAGATGCTGCACTTAATCTGCAAGCAGTGAAGT 666  
Db 601 CTCACAAATCAGCAGATGAGGCTGAAGATGCTGCACTTAATCTGCAAGCAGTGAAGT 660  
QY 667 AGTAACCACTCAAGTGTGGTGTGGGACCAAGCTGAGAGCTGAAACG 713  
Db 661 AGTAACCACTCAAGTGTGGTGTGGGACCAAGCTGAGAGCTGAAACG 707

RESULT 13  
LOCUS AR051416 711 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 64 from patent US 5830663.  
ACCESSION AR051416  
VERSION AR051416.1 GI:5974780  
KEYWORDS  
SOURCE unknown.  
ORGANISM unknown.  
REFERENCE 1 (bases 1 to 711)  
AUTHORS Emblemson, M.J., Gorochoy, G., Jones, P.T. and Winter, G.P.  
TITLE In situ recombinant PCR within single cells  
JOURNAL Patent: US 5830663-A 64 03-NOV-1998;  
FEATURES  
source location/Qualifiers  
1..711  
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ORIGIN

Query Match 68.5%; Score 651; DB 6; Length 711;  
Best Local Similarity 95.0%; Pred. No. 7.1e-163;  
Matches 672; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
QY 7 GAGGTCAAGCTCAGAGAGTCAAGGAGGCTTAAGTCAAGGCTCGAGGGTCCCGGAAACTC 66  
Db 1 GATGTGCAAGCTGTGAGAGTCTGGGGAGGCTTAAGTCAAGGCTCGAGGGTCCCGGAAACTC 60  
QY 67 TCCTGTGAGCCTCTGAGATTCATTTCAAGTACCTTTGGAATGCACTGGGTTGTCAGAGCT 126  
Db 61 TCCTGTGAGCCTCTGAGATTCATTTCAAGTACCTTTGGAATGCACTGGGTTGTCAGAGCT 120

QY 127 CCAGAGAGGGGCTGGAGTGGGTGCGATATATTAGTGGCAGTACATCTACTAT 186  
DB 121 CCAGAGAGGGGCTGGAGTGGGTGCGATATATTAGTGGCAGTACATCTACTAT 180  
QY 187 GGAGACACAGTGAAGGAGCATTCACCATCTCCAGAGCAATCCCAAGAACACCTGTTT 246  
DB 181 GGAGACACAGTGAAGGAGCATTCACCATCTCCAGAGCAATCCCAAGAACACCTGTTT 240  
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QY 547 AAATGTCTTTTGGAGATCCCTGCTTCAAGTGGAGTGGGTCTGGACCTTTACTCT 606  
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QY 607 CTCACAAATGACGAGTGAAGGCTGAAGATGTGCCACTTAATCTGCCAGAGTGAAGT 666  
DB 601 CTCACAAATGACGAGTGAAGGCTGAAGATGTGCCACTTAATCTGCCAGAGTGAAGT 660  
QY 667 AGTAACCACTACGTTCCGTGCTGGAGCAACAGCTGAGCTGAACG 713  
DB 661 AGTAACCACTACGTTCCGTGCTGGAGCAACAGCTGAGCTGAACG 707

RESULT 14  
A25746 672 bp DNA linear PAT 14-MAR-1995  
LOCUS Variable region heavy and kappa light chain linked genes (stage 2).  
DEFINITION A25746  
ACCESSION A25746  
VERSION A25746.1 GI:904740  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 672)  
TREATMENT OF CELL POPULATIONS  
AUTHORS Patent: WO 9303151-A 57 18-FEB-1993;  
JOURNAL Location/Qualifiers  
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source 1..672  
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ORIGIN  
Query Match 61.1%; Score 580.6; DB 6; Length 672;  
Best Local Similarity 91.1%; Pred. No. 4.8e-144;  
Matches 644; Conservative 0; Mismatches 24; Indels 39; Gaps 1;

QY 7 GAGTCAAGCTCAGAGTGCAGGGGAGGCTTATGTCAGGCTGGAGGGTCCGGAATCTC 66  
DB 1 GAGTCAAGCTCAGAGTGCAGGGGAGGCTTATGTCAGGCTGGAGGGTCCGGAATCTC 60  
QY 67 TCTGTGACAGCCTCTGGATTCATCTTCAGTACCTTTGGAATGACATGGGTGGTCAAGGCT 126  
DB 61 TCTGTGACAGCCTCTGGATTCATCTTCAGTACCTTTGGAATGACATGGGTGGTCAAGGCT 120  
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DB 301 GGGGCTTATTGGGGCCAAAGGAGACACGATCACCCTCTCTCAGTGGAGGCGGCTCAGGC 360  
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LOCUS Sequence 62 from patent US 5830663.  
DEFINITION AR051415  
ACCESSION AR051415  
VERSION AR051415.1 GI:5974779  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 672)  
AUTHORS Embleton,M.J., Gorochoy,G., Jones,P.T. and Winter,G.P.  
JOURNAL In situ recombinant PCR within single cells  
TITLE Patent: US 5830663-A 62 03-NOV-1998;  
FEATURES  
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ORIGIN  
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Db 181 GCAGACACAGTGAAGGAGGAGATTCAACATCTCCAGAGACATCCCAAGAACCTCTTTC 240
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Search completed: June 23, 2005, 09:03:47  
Job time : 6828 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: June 23, 2005, 05:58:45 ; Search time 3730 Seconds  
(without alignments)  
9704.858 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_esc2:\*  
3: gb\_hic:\*  
4: gb\_esc3:\*  
5: gb\_esc4:\*  
6: gb\_esc5:\*  
7: gb\_esc6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 2	356.8	37.5	601	5	BO474958 CARB849
C 3	354.6	37.3	1104	7	CK629846 AM2-AA002
C 4	335.4	35.3	1339	7	CK629414 AM1-AA001
C 5	334.2	35.1	1419	7	CK629415 AM1-AA001
C 6	332.6	35.0	498	2	BF857861 QV1-FT020
C 7	328.2	34.5	488	2	BF857860 QV1-FT020
C 8	324	34.1	476	2	BF923394 QV4-MT024
C 9	322.6	33.9	452	4	BI055323 RC0-GN023
C 10	311.2	32.7	585	4	BI030095 IL0-MT035
C 11	309.8	32.6	416	4	BI025870 IL0-MT036
C 12	309.8	32.6	419	5	BO321312 RC0-CT047
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C 15	309.8	32.6	445	5	BO321751 MR1-CT052
C 16	309.8	32.6	449	5	BO372280 RC0-EN018
C 17	309.8	32.6	460	5	BO321747 MR1-CT052
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C 19	309.8	32.6	462	4	BI030046 IL0-MT034
C 20	309.8	32.6	464	4	BI043086 QV1-CT017
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C 22	308.8	32.5	473	5	BO328151 MR4-RT004
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C 28	308.2	32.4	424	5	BO376239 MR4-TN010
C 29	308.2	32.4	459	4	BI025872 IL0-MT036
C 30	307.8	32.4	454	2	BF894857 QV1-MT016
C 31	307.2	32.3	458	4	BI029994 IL0-MT034
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C 33	306.6	32.2	455	4	BI030044 IL0-MT034
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## ALIGNMENTS

RESULT 1  
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DEFINITION AMO-AA0013-110902-011-H03 AA0013 Apis mellifera cDNA, mRNA  
sequence.  
ACCESSION CK629396  
VERSION CK629396.1 GI:45753871  
KEYWORDS EST.  
SOURCE Apis mellifera (honey bee)  
ORGANISM Apis mellifera  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata; Apoidea; Apidae; Apis.

REFERENCE 1 (bases 1 to 872)  
AUTHORS Nunes,F.M.F., Valente,V., Sousa,J.F., Cunha,M.A.V., Pinheiro,D.G., Mala,R.M., Araujo,D.D., Costa,M.C.R., Martins,W.K., Carvalho,A.F., Monesi,N., Nascimento,A.M., Peixoto,P.M.V., Silva,M.F.R., Ramos,R.G.P., Reis,L.F.L., Dias Neto,E., Souza,S.J., Simpson,A.J.G., Zagro,M.A., Soares,A.E.E., Bitondi,M.M.G., Espresifco,E.M., Espindola,F.S., Peco-Larson,M.L., Simoes,Z.L.P., Hartfelder,K. and Silva,W.A., Jr.  
Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome  
Unpublished (2004)  
Contact: Silva Jr. W. A.

COMMENT  
Molecular Genetic and Bioinformatics Laboratory  
Department of Genetics, FMRP/USP, FUNDHERP  
Rua Tenente Catão Roxo, 2501, CEP 14051-140, Brazil  
Tel: +55 16 39639300  
Fax: +55 16 39639309  
Email: wilsonjr@usp.br  
This sequence was derived from the FAPESP Genome Program  
High quality sequence start: 66  
High quality sequence stop: 625.  
Location/Qualifiers  
1..872  
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## FEATURES

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## ORIGIN

Query Match

38.3%; Score 364.2; DB 7; Length 872;



REFERENCE	1 (bases 1 to 1104)
AUTHORS	Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Mata, R.M., Kruijo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Ramest, N., Nascimento, A.M., Teixeira, P.M.V., Silva, M.F.R., Ramos, R.G.P., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Depaeafico, E.M., Espindola, F.S., Peco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, M.A. Jr.
TITLE	Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome
JOURNAL	Unpublished (2004)
COMMENT	Contact: Silva Jr., W. A. Molecular Genetic and Bioinformatics Laboratory Department of Genetics, FMRP/USP, RUMBERP Rua Tenente Celso Roxo, 2501, CEP 14051-140, Brazil Tel.: +55 16 39639300 Fax: +55 16 39639309 Email: wilsonjr@usp.br This sequence was derived from the FAPESP Genome Program High quality sequence start: 64 High quality sequence stop: 594.
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Db	745 GCTTCTTGCTACATCTTCACAGATTATATATAGACTGTTGAGGACACCGCTGACAA 686
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Db	685 GGACTTGAGTGAATGGATGATTTTTCGTGAGAGGGGAGTACTGAATCAATGAGAA 626
Db	195 AGTAGAGGAGCATTCACATCTCCAGAGACATCCCAAGAACCCCTGTTCTGCAAT 254
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Db	255 GACCAAGTATAGTCTGAGGACACGGGTATGATTTACTGTGCAAGATTAACG----- 308
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Db	505 GCGCTACTTTGACTGTGGGGGCCAAAGGAGACACAGCTCAAGCTCTCTCATGTGAGACG 446
Db	359 GCTCAGGGGAGGTGGCTCTGGCGGTGGCGGATCGGACATTTGAGTCAACCAAGTCTCCAG 418
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DEFINITION			AA1-AA00014-041102-021-H09	AA0014	Apl <sup>s</sup> mellifera cDNA, mRNA		
SEQUENCE:			sequence.				

ORGANISM	Apis mellifera
SOURCE	Apis mellifera (honey bee)
KEYWORDS	EST.
VERSION	CK629415.1
ACCESSION	GI:45753890
CK629415	

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Apocrita; Aculeata; Apoidea; Apidae; Apis.

## REFERENCE AUTHORS

TITLE  
Open reading frame ESTs - an efficient strategy for analysis of the  
honey bee transcriptome

JOURNAL  
COMMENT

Molecular Genetic and Bioinformatics Laboratory  
Department of Genetics, FMRP/USP, FUNDHERP  
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil  
Tel.: +55 16 30630300

Tel: +55 16 33632309  
 Fax: +55 16 33633039  
 Email: wilsonjr@usp.br  
 This sequence was derived from the FAPESP Genome Program  
 High quality sequence start: 63  
 High quality sequence stop: 605.

**FEATURES**

**SOURCE**

Location/Qualifiers  
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BF857861				

ACCESSION	BF857861
VERSION	BF857861.1
KEYWORDS	GI:12245605
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ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 498)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,

**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, São Paulo-SP,  
Brazil



Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV1&t2=QV1-FT0202-071100-465-f03&t3=2000-11-07&t4=1>)  
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 Location/Qualifiers

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## ORIGIN

Query Match 35.0%; Score 332.6; DB 2; Length 498;  
 Best Local Similarity 88.1%; Pred. No. 1.8e-80;  
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RESULT 7  
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 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 488)  
 Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT  
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 10737800  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV1&t2=QV1-FT0202-071100-465-f03&t3=2000-11-07&t4=1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 8  
 High quality sequence stop: 487.  
 Location/Qualifiers

## FEATURES

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 /note="Organ: prostate tumor; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 34.5%; Score 328.2; DB 2; Length 488;  
 Best Local Similarity 88.1%; Pred. No. 2.9e-79;  
 Matches 357; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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 QY 382 GGTGGGATCGGACATTGAGTCAACCACTCCAGCATCATGTGATCTCCAGG 441  
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 QY 442 GAGAGGTCACATGACCTGCGAGTGCAGTTCAAGTGTAAAGTACATGAATGTTCCAA 501  
 DB 368 GAGAGGTCACATGACCTGCGAGTGCAGTTCAAGTGTAAAGTACATGAATGTTCCAA 309  
 QY 502 CAGAAGTCAGGACCTCCGCCAAAGATGATTATGACATCCAAATGTCTTGGG 561  
 DB 308 CAGAAGTCAGGACCTCCGCCAAAGATGATTATGACATCCAAATGTCTTGGG 249  
 QY 562 GTCCCTGCTGCTTCACTGAGTGGGTCTGGGACCTCTTACTCTTCAATCAGAGC 621  
 DB 248 GTCCCTTTCGCTTCACTGAGTGGGTCTGGGACCTCTTACTCTTCAATCAGAGC 189  
 QY 622 ATGAGAGCTGAAGATGCTGCTTCACTTCTGCGAGCATGAGTGTAAAGTACATGAATCAG 661  
 DB 188 ATGAGAGCTGAAGATGCTGCTTCACTTCTGCGAGCATGAGTGTAAAGTACATGAATCAG 129  
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DEFINITION	QV4-NR0248-271100-585-cl0 NR0248 Homo sapiens CDNA, mRNA sequence.
ACCESSION	BFe923394
VERSION	BFe923394.1   GI:12319282
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 476) Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,... Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matukuma,A., Bala,G.S., Simpson,D.H.,... Brunser,J., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J. Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE PUBMED COMMENT	10737800 Contact: Simpson A.J.G.

**FEATURES**  
**Source**  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=QV4&t2=QV4-NT0248.271100-585-cl0ec3=2000-11-27&t4=1>  
 Seq primer: puc 18 forward  
 High quality sequence start: 42  
 High quality sequence stop: 395.  
 Location/Qualifiers  
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ORIGIN

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QY	376	TCGTGCGGTGGCGGAT	TGGACATTGAGTCA	CCAGTCTCCAGCAATATATGTGCACCT	435
Db	406	TCGTGCGGTGCGAAT	TGCAATTGAGTCA	CCAGTCTCCAGCAATATATGTGCACCT	347
QY	436	CCAGGGGAGAGGTTC	ACCATGACCTGTG	AGTCCAGTTCAAGTGTAAAGTACATGAACATGG	495
Db	346	CCAGGGGAGAGGTTC	ACCATGACCTGTG	AGTCCAGTTCAAGTGTAAAGTACATGAACATGG	287
QY	496	TTCCAAACAAGAGTCA	AGGACCTCCCC	CCAAAAGATGATTTATGACATCTCCAAACTGCT	555
Db	286	TATCCAAACAAGAGT	CAATCTCTCCCC	CCAGATCTCTGATTTATGACATCTCCAGAGTGGCT	227

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556	CTGTGAGTCCCTGTCGCGCTTGAAGGACAGTGGGTGTGGGAACTCTTATCTCTCAAAAC	616	AGCAGCATTGAGAGGCTGAGATGCTGCCACTTA
226	CTGTGAGTCCCTGTCGCGCTTGAAGGACAGTGGGTGTGGGAACTCTTATCTCTCAAAAC	166	TACCGAATGAGGCTGAGAGTCTGCCACTTATTA
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		106	TACACGTTCCGAGGGGGGACCAAGCTGAGGCTGAACGGGCGGC

RESULT 9			
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ACCESSION	BI055323		linear mRNA sequence.
VERSION	BI055323.1	GI:14462853	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	COMMENT
1 (bases 1 to 452)	Dias Neto, E., Garcia Correa, R., Veijovicki-Almeida, S., Briones, M. R., Nagaï, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brustein, A. E., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A.	97 (7), 3491-3496	(2000)	
				20202663		
				10737800		Contact: Simpson A.J.G.

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Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
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Project. This entry can be seen in the following URL:  
<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC06ct2-RC0-GN0233-060201-011-B08ct3-2001-02-06ct4-1>  
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High quality sequence start: 42  
High quality sequence stop: 452.  
Location/Qualifiers

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/notes="Organ: placenta.normal; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN
Query Match
Best Local Similarity 88.8%; Pred. No. 9.9e-78; Length 452;
Matches 349; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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Db 392 GACATTGAGCTACCCAGTCTCCAGCAATCATCTGCATCTCCAGGGAGAGGCTCAC 333  
Oy 454 ATGACCTGACGTGCGCAGTTCAAGTGTAACTGATCACTGATCTCCAGCAAGAGTCA 513  
Db 332 ATGACCTGACGTGCGCAGTTCAAGTGTAACTGATCACTGATCTCCAGCAAGAGTCA 273  
Oy 514 ACCTCCCGCAAAAGATGATTTTGTACATCCAACTGCTTCTGTGAGTCCCTGCTCG 573  
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Db 152 GATGCTGCACCTTACTACTGCGCAGAGTGAATGTAACCACTCACTGCTGCTGAG 93  
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Db 92 ACCAAGCTGAGCTGAAACGGGCGCGCGAGAA 60

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DEFINITION B1030095  
VERSION B1030095.1 GI:14436725  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 585)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL0&ct=IL0-MT0355-  
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## FEATURES

source

/note="Organ: marrow; Vector: puc18; Site\_1: Sma1; Site\_2:  
Sma1; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No.  
196,716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

ORIGIN  
Query Match 32.7%; Score 311.2; DB 4; Length 585;  
Best Local Similarity 85.8%; Pred No. 1.5e-74;  
Matches 357; Conservative 0; Mismatches 58; Indels 1; Gaps 1;

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VERSION B1025870.1 GI:14432500  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 416)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=IL0&l2=IL0-MT0364-050201-500-501&l3=2001-02-05&l4=1>)

Seq primer: puc 18 forward  
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Location/Qualifiers

## FEATURES

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## ORIGIN

Query Match 32.6%; Score 309.8; DB 4; Length 416;  
Best Local Similarity 88.9%; Pred. No. 3.3e-74;  
Matches 335; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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355 AGCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGGTCAACATGACCTGAGTCCA 296
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55 AACGGGCGGCGCGCAGAA 39
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ACCESSION BQ321312  
VERSION BQ321312.1 GI:20929288  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
1 (baes 1 to 419)  
Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Brijones, M.R.,  
Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, J., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

TITLE Simpson, A.J.  
JOURNAL Shotgun sequencing of the human transcriptome with ORF expressed  
PROC. NATL. ACAD. SCI. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC0&l2=RC0-CT0472-080800-031-f01&l3=2000-08-08&l4=1>)

## FEATURES

Source

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/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
```

## ORIGIN

Query Match 32.6%; Score 309.8; DB 5; Length 419;  
Best Local Similarity 88.9%; Pred. No. 3.3e-74;  
Matches 335; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

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350 GTGAGGCGGCTCAGCGAGGCTCTGCGCGTGGCGATCGACATTGAGCTCACC 409
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DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS	TITLE
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JOURNAL MEDLINE PUBMED	20202663	10737800	Contact: Stimpson A.J.G.	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
COMMENT						

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
 This sequence was derived from the PAPSP/ICR Human Cancer Genome Project. This entry can be seen in the following URL  
<http://www.ludwig.org.br/bcscripts/gethtml2.pl?rl=RC3&t2=RC3-BN0428-201100-011-f06&t3=2000-11-1-20&t4=1>  
 Seq primer: puc 18 forward  
 High quality sequence start: 34  
 High quality sequence stop: 427.  
 Location/Qualifiers  
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/mol_type="mRNA"
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/dev_stage="Adult"
/clone_1lb="BN0428"
/notes="Organ: breast normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

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	Matches	335	Conservative	0	Mismatches	42	Indels	0	Gaps	0
QY	350	GTGAGGCGGCTCAGGCGGAGGTGAGCTTGGCGGTGGCGGATTCGACATTGAGCTCACCC	409							
Db	426	GTGAGGCGGCTTACAGGCGGAGGTGAGCTTGGCGGTGGCGGATTCGACATTGAGCTCACCC	367							
QY	410	AGTTCACAGCATATGTCTGCAATCTCAGGGGAGAGGGTCAACATAGACTTCGACATGCCA	469							
Db	366	AGTTCACAGCATATGTCTGCAATCTCAGGGGAGAGGGTCAACATAGACTTCGACATGCCA	307							
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QY	530	GGATTTATGACATCCAAACTGCTTCCTGAGAGTCCCTGCTCGCTTCAGTGGCAGTGGGT	589							
Db	246	TGATTTATGACATCCAAAGTGGCTCTGGAGAGTCCCTTTTCGCTTCAGTGGCAGTGGGT	187							
QY	590	CTGGGACCTCTTAATCTCTACATTCAGCAGATGAGAGGCTGMAAGTCTGCCATTACT	649							

Db	186	CTGGGACCTTATTCTCTCAACATCAACCGAATGAGAGGCTGAGAGATGCTGCCACTTATT	127
QY	650	ACTGCCAGCAGTGAAGTAAACCCACTCAAGTTCGATGCTGGGACCAAGCTGGAGCTGA	709
Db	126	ACTGCCAGAGTGAAGTGTATTCCGTACACGTTTCGAGGGGGGACCAACTGAGCTGA	67
QY	710	AACGGCGCGCCGCGAGAA	726
Db	66	AACGGCGCGCCGCGAGAA	50

RESULT	14
LOCUS	B0321307/c
DEFINITION	B0321307 437 bp mRNA linear EST 17-MAY-2002
ACCESSION	R03-CT0402-080800-031.d01 CTr472 Homo sapiens cDNA, mRNA sequence.
VERSION	B0321307
KEYWORDS	B0321307.1 GI:20929277
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Homo sapiens

REFERENCE  
1 (bases 1 to 437)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., et al. (2005) A new approach to the analysis of the human genome. *Genomics* 85: 103-112.

**TITLE**  
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and  
Simpson, A. J.  
Stopgun sequencing of the human transcriptome with ORF expressed  
sequence tags

JOURNAL.  
PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE  
20202663  
PUBMED  
10737800  
COMMENT  
Contact: Simpson A.J.G.

**FEATURES**  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel.: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: aaimp@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (<http://www.ludwig.org.br/bcrlp/s/gethtml2.pl?tl=RC0at2-RC0-CT0472-080800-031-d01ct3=2000-08-08&ct=1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 38  
 High quality sequence stop: 437.  
 Location/Qualifiers

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/organism="Homo sapiens"
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/dev_stage="Adult"
/clone_id="CT0472"
/notes="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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ORIGIN	Query Match	32.6%;	Score 309.8;	DB 5;	Length 437;
	Best Local Similarity	88.9%;	Pred. No. 3.4e-74;		
	Matches 335;	Conservative	0;	Mismatches 42;	Indels 0;
				Gaps	0;
QY	350	GTGAGGCGGCTCAGAGCGGAGGTGCTCTGCGCGGTGCGGATGCGACATTGAGCTCACCC	409		
Db	436	GTGAGGCGGCTTACGAGCGAGGTGCTCTGCGCGGTGCGGATTCGACATTGAGCTCACCC	377		

QY 410 AGCTCCAGCAATCATGTCGATCTTCACAGGGAGAGGGTCCATCATGACCTGACGTGCCA 469  
DB 376 AGCTCCAGCAATCATGTCGATCTTCACAGGGAGAGGGTCCATCATGACCTGACGTGCCA 317  
QY 470 GTTCAAGTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529  
DB 316 GCTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 257  
QY 530 GGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 589  
DB 256 TGAATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 197  
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DB 196 CTGGAGCCTTACTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 137  
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DB 136 ACTGCCAGCAGTGAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGAT 77  
QY 710 AACGGCGCGCGCAGAA 726  
DB 76 AACGGCGCGCGCAGAA 60

RESULT 15  
BQ321751/c 445 bp mRNA linear EST 17-MAY-2002  
LOCUS MR1-CT0529-250900-003-d01 CT0529 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BQ321751  
ACCESSION BQ321751  
VERSION BQ321751.1 GI:20930355  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 445)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,  
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
PUBMED 10737800  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR1&f2=MR1-CT0529-  
250900-003-d01&t3=2000-09-25&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 22  
High quality sequence stop: 445.  
Location/Qualifiers

## FEATURES

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/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:  
SmaI; A mini-library was made by cloning products derived  
from ORFESTS PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

ORIGIN  
Query Match 32.6%; Score 309.8; DB 5; Length 445;  
Best Local Similarity 88.9%; Pred. No. 3.4e-74;  
Matches 335; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
QY 350 GTGAGGCGGCTCAAGCGGAGGATGATGATGATGATGATGATGATGATGATGATGAT 409  
DB 444 GTGAGGCGGCTCAAGCGGAGGATGATGATGATGATGATGATGATGATGATGATGAT 385  
QY 410 AGTCTCCAGCAATCATGTCGATCTTCACAGGGAGAGGGTCCATCATGACCTGACGTGCCA 469  
DB 384 AGTCTCCAGCAATCATGTCGATCTTCACAGGGAGAGGGTCCATCATGACCTGACGTGCCA 325  
QY 470 GTTCAAGTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529  
DB 324 GCTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 265  
QY 530 GGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 589  
DB 264 TGAATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 205  
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DB 204 CTGGAGCCTTACTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 145  
QY 650 ACTGCCAGCAGTGAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGAT 709  
DB 144 ACTGCCAGCAGTGAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGAT 85  
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DB 84 AACGGCGCGCGCAGAA 68

Search completed: June 23, 2005, 10:06:04  
Job time : 3735 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: June 23, 2005, 05:54:00 ; Search time 613 seconds  
(without alignments)  
9183.808 Million cell updates/sec

Title: US-09-403-882A-1  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: geneseqn1980a:\*  
2: geneseqn1990a:\*  
3: geneseqn2000a:\*  
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5: geneseqn2001b:\*  
6: geneseqn2002a:\*  
7: geneseqn2002b:\*  
8: geneseqn2003a:\*  
9: geneseqn2003b:\*  
10: geneseqn2003c:\*  
11: geneseqn2003d:\*  
12: geneseqn2004a:\*  
13: geneseqn2004b:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	951	100.0	951	2	AAZ20266	AAZ20266 cDNA codi
2	949	99.8	8902	4	AAH78812	AAH78812 Candidate
3	934.4	98.3	6115	2	AAH63235	AAH63235 Eukaryot
4	749.6	78.8	1256	3	AAAG6074	AAAG6074 E. coli e
5	749.6	78.8	1256	4	AAAF7806	AAAF7806 Fragment
6	749.6	78.8	1256	4	AAAF6193	AAAF6193 Expressio
7	749.6	78.8	1256	5	AAAD0212	AAAD0212 Partial p
8	737	77.5	843	9	ACC84876	ACC84876 Single-ch
9	699.4	73.5	726	6	AAK98639	AAK98639 scFv anti
10	655.4	68.9	738	2	AAO80468	AAO80468 Single ch
11	651	68.5	711	2	AAO37461	AAO37461 VH NQ10/1
12	580.6	61.1	672	2	AAO37460	AAO37460 VH NQ10/1
13	548	57.6	1725	2	AAAO1651	AAAO1651 Bispecific
14	539	56.7	1668	2	AAAO1652	AAAO1652 Bispecific
15	532.4	56.0	711	9	AAAD5807	AAAD5807 Mouse G1
16	510	53.6	738	10	ADL08398	ADL08398 Microsome
17	510	53.6	1157	10	ADL08390	ADL08390 Microsome
18	474.4	49.9	774	2	AAAO1655	AAAO1655 Anti-B7.1
19	470	49.4	841	10	AAAC57514	AAAC57514 Newcastle
20	468.6	49.3	807	3	AAZ50508	AAZ50508 Recombina

21	467	49.1	927	5	AAAF61510	AAAF61510 DNA encod
22	465	48.9	888	4	AAAF30732	AAAF30732 DNA encod
23	462.8	48.7	708	2	AAO37459	AAO37459 VH NQ2/12
24	462.2	48.6	870	2	AAAT7009	AAAT7009 Intracell
25	461.2	48.5	840	3	AAAO8033	AAAO8033 Antibody
26	460.6	48.4	807	3	AAZ50509	AAZ50509 Recombina
27	460.2	48.4	807	3	AAZ28963	AAZ28963 Anti-Hepa
28	460.2	48.4	807	13	ADSO8281	ADSO8281 Human ant
29	459.6	48.3	703	12	ADNO7019	ADNO7019 Human SC
30	453.2	47.7	872	2	AAO76287	AAO76287 OMVU10 Bc
31	452	47.5	756	12	ADH77286	ADH77286 Yeast k11
32	449.6	47.3	1679	2	AAAF58130	AAAF58130 Single ch
33	449.6	47.3	1679	2	AAV08176	AAV08176 H22-anti-
34	449.6	47.3	1679	5	AAAC85183	AAAC85183 Bispecific
35	449.6	47.3	1679	5	AAH23383	AAH23383 Bispecific
36	448.8	47.2	726	6	ACC83315	ACC83315 Single ch
37	448.8	47.2	726	13	ADP91208	ADP91208 Single ch
38	446	46.9	759	2	AAAO1659	AAAO1659 Anti-B7.1
39	446	46.9	861	12	ADNO7014	ADNO7014 Human EFG
40	445.4	46.8	810	13	ADSO17526	ADSO17526 Nucleotid
41	444.2	46.7	717	2	AAAT7246	AAAT7246 Mouse scF
42	442	46.5	717	4	AAAC85539	AAAC85539 scFv 508F
43	442	46.5	717	10	AAAL51099	AAAL51099 Human neu
44	442	46.5	717	12	ADSO88112	ADSO88112 Human det
45	438.2	46.1	720	6	AAAD2824	AAAD2824 KOR bindi

## ALIGNMENTS

RESULT 1	AAZ20266	AAZ20266 standard; cDNA; 951 BP.
ID	AAZ20266	
XX	AAZ20266;	
AC	17-JUN-2000 (first entry)	
DT		
XX		
DE	cDNA coding single chain antibody used in probe detection.	
XX		
XX	Single chain antibody; scAb; scFv; spectroscopic probe; ss.	
XX		
OS	Unidentified.	
XX		
PN	MO9951986-A1.	
XX		
PD	14-OCT-1999.	
XX		
PF	08-APR-1999; 99MO-US007847.	
XX		
PR	08-APR-1998; 98US-0081118P.	
PR	09-APR-1998; 98US-0081340P.	
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX		
PI	Farinas J;	
XX		
DR	WPI; 1999-611066/52.	
XX	P-PDB; AAY32086.	
PT	Localizing probes to specific sites in cells that express single-chain antibody reactive with probe-ligand conjugate, particularly for detecting post-translational modification and its modulators.	
XX		
PS	Disclosure; Page 47-48; 69pp; English.	
XX		
CC	This cDNA codes for a single chain antibody (scAb, see AAY32086) that has 2 c-myc epitopes. The cDNA can be amplified from plasmid pHook-1 by PCR (see also AAZ20267-68). The scAb is used in claimed methods for localizing a probe and for detecting a post-translational activity in a cell, and is expressed by a claimed transgenic non-human animal. The invention provides methods and reagents for targeting probes to selected cellular locations through the expression of specific binding partners	
CC		

CC (such as scAbs) within a cell, and for creating assays for post-translation activities. The invention allows the monitoring of the location of such intracellular, specific binding partners over time and in response to stimuli, such as test chemicals. Spectroscopic probes can be used to screen a test chemical for activity. The invention also includes cells and transgenic organisms comprising the intracellular specific binding partner, where the specific binding partner can bind with the spectroscopic probe/ligand conjugate. scAbs can be expressed within the cell and can be designed to bind a wide variety of spectroscopic probes, including small molecules that have better (and more diverse) spectroscopic properties than green fluorescent protein

XX Sequence 951 BP; 226 A; 247 C; 272 G; 206 T; 0 U; 0 Other;

Query Match 100.0%; Score 951; DB 2; Length 951;  
Best Local Similarity 100.0%; Pred. No. 1.1e-242;  
Matches 951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGGCCGAGTCAAGTGCAGAGTCAAGGGGAGGCTTATGTCAGCTTGGAGGGTCCCG 60
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QY 61 AAATCTCTGTGACAGCTCTGGAATTCATTTCAGTAGCTTGGAAATGCACTGGGTGGT 120
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QY 481 AGGTACATGAACTGTTCCCAACAGAAATGACGACCTCCCAAAAGATGATTTATGAC 540
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QY 901 ATCATCTCCCTTATATCTCATCTATCTGTTTGGCAGAAAGCCACGTTAG 951
DB 901 ATCATCTCCCTTATATCTCATCTATCTGTTTGGCAGAAAGCCACGTTAG 951

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# RESULT 2

AAH78812  
ID AAH78812 standard; DNA; 8902 BP.

AAH78812;  
03-MAY-2002 (first entry)

DE Candidate peptide inhibitor expressing plasmid vector (pBLOCK-3-8).

KW Reverse n-hybrid screening method; pBLOCK-3.8 plasmid vector; de;  
KW biological antagonist; biological inhibitor; peptide inhibitor;  
KW common binding partner; leukaemia; solid tumour.

OS Synthetic.

XX WO20016787-A1.

PD 13-SEP-2001.

PF 08-MAR-2001; 2001WO-US007669.

PR 08-MAR-2000; 2000AU-00006131.

PR 23-MAR-2000; 2000AU-00006437.

PR 11-APR-2000; 2000AU-00006830.

PR 06-NOV-2000; 2000AU-00001256.

PA (TWNT-) TWN TELETHON INST CHILD HEALTH RES.

PI Hopkins R, Serebriiskii I, Watt PM, Golemis E;

DR WPI; 2001-582279/65.

PT Screening antagonist or inhibitor of biological interaction, by improved  
PT reverse n-hybrid screening utilizing multiple genes to distinguish  
PT antagonists or inhibitors of one interaction from that of other  
PT interactions.

PS Claim 47; Page 93-98; 125pp; English.

XX The invention comprises a reverse n-hybrid screening method for  
CC identifying antagonists or inhibitors of biological interactions. The  
CC method involves the use of multiple genes to distinguish antagonists or  
CC inhibitors of one interaction from those of other interactions. The  
CC method identifies peptides which inhibit a target interaction (between at  
CC least two binding partners), but does not inhibit a non-target  
CC interaction within a host cell. The method further comprises a series of  
CC plasmid vectors designed to express candidate peptide inhibitors. The  
CC method of the invention has enhanced specificity in the detection of  
CC interacting binding partners compared to conventional reverse n-hybrid  
CC screens. The method of the invention also has the capacity to distinguish  
CC between interactions that involve one or more common binding partners.  
CC The method of the invention is useful for identifying a peptide which  
CC inhibits a target interaction. The peptides identified by the method of  
CC the invention may be used in the treatment of leukaemia and solid  
CC tumours. The present sequence represents a plasmid vector (pBLOCK-3.8) of  
CC the invention that is designed to express a candidate peptide inhibitor  
XX

Sequence 8902 BP; 2200 A; 2201 C; 2134 G; 2365 T; 0 U; 2 Other;

Query Match 99.8%; Score 949; DB 4; Length 8902;  
Best Local Similarity 99.8%; Pred. No. 8.2e-242;  
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



QY	ATGCGCGAGGCTCAAGCTGCAGAGAGTCAGGGGAGAGGCTTAAGTCAGACGCTGCAGAGGGTCTCCGG	60
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QY	AAACTCTCTCTGCGAGCCTCTGGAATTCACCTTTCAGTAGCTTTGGAAATGCATCTGGGTTTGGT	61
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QY	CAGGCTCCAGAGAAAGGGGCTGAGAGTGGGTGGCATATATATTAGTAGTGGCAGTAGTACATC	121
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QY	TACTATGTCAGACACAGTGAAGGAGACGATTCACATCTCCAGAGCAATATCCCAAGAACACC	181
Db	TACTATGTCAGACACAGTGAAGGAGACGATTCACATCTCCAGAGCAATATCCCAAGAACACC	3000
QY	CTGTTCCTGCAAAATGACACGATCTAAGGCTGTAGAGCAGCGGTCATGATATTACTGTGCAGAA	241
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QY	GATTACGGGGCTTATTTGGGGCCAAAGGGACCAACGGTCACCGTCTCTCCAGGTGAGAGCGGC	301
Db	GATTACGGGGCTTATTTGGGGCCAAAGGGACCAACGGTCACCGTCTCTCCAGGTGAGAGCGGC	3120
QY	TCAGGCGGAGGTGGGCTCTGGGGGTCGGGGGATTCGAGCATTTGAGGTCACCACTTCACGACA	361
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QY	ATCATATGTCGATCTCCAGGGGAGAGGGTTCACATATGACTGTGACGTCAGTTCACAAAGTGA	421
Db	ATCATATGTCGATCTCCAGGGGAGAGGGTTCACATATGACTGTGACGTCAGTTCACAAAGTGA	3240
QY	AGGTACATGAATCTGGTTCACACAGAGTCAGGCACCTTCCCAAAAGATGATTTATGAC	481
Db	AGGTACATGAATCTGGTTCACACAGAGTCAGGCACCTTCCCAAAAGATGATTTATGAC	3300
QY	ACATCCCAAACGTCTTCTTGAGAGTCCCTGCTGGCTTCAATGAGCAGTGGGTCTGGGACCTCT	541
Db	ACATCCCAAACGTCTTCTTGAGAGTCCCTGCTGGCTTCAATGAGCAGTGGGTCTGGGACCTCT	3360
QY	TACTCTCTCACAAATCAGCAGATGAGAGGCTGAAGATGTGTGCACCTTACTGTGCAGAG	601
Db	TACTCTCTCACAAATCAGCAGATGAGAGGCTGAAGATGTGTGCACCTTACTGTGCAGAG	3420
QY	TGAGTAGTAAACCACTCAGCTTGGTGTCTGAGACCAAGCTGAGACTGAAACGGCGGCGC	661
Db	TGAGTAGTAAACCACTCAGCTTGGTGTCTGAGACCAAGCTGAGACTGAAACGGCGGCGC	3480
QY	GCAGAACAAAAATCTCATCTCAGAAAGAGATCTGAATGGGGCCGTGTGACGAACAAAAATCT	721
Db	GCAGAACAAAAATCTCATCTCAGAAAGAGATCTGAATGGGGCCGTGTGACGAACAAAAATCT	3540
QY	ATCTCAGAAAGAGATCTGAATGCTGTGGGCCAGGACGACAGAGAGTCATGCTGTGGTGC	781
Db	ATCTCAGAAAGAGATCTGAATGCTGTGGGCCAGGACGACAGAGAGTCATGCTGTGGTGC	3600
QY	CACCTCTTGCCCTTTAAGGTGGTGTGATCTCAGGCATCTTGCCCTGTGTGTGTCTCAC	841
Db	CACCTCTTGCCCTTTAAGGTGGTGTGATCTCAGGCATCTTGCCCTGTGTGTGTCTCAC	3660
QY	ATCATATCTCCCTTATCATCTCATCATATGCTTTGGCAGAAAGAACCCAGTTAG	901
Db	ATCATATCTCCCTTATCATCTCATCATATGCTTTGGCAGAAAGAACCCAGTTAG	3720

RESULT 3	
AAT63235	
ID	AAT63235 standard; DNA; 6115 BP
XX	
AC	AAT63235;
XX	
DT	27-AUG-2003 (revised)

DT	18-JUN-1997	(first entry)
XX	Eukaryotic expression vector plasmid pPhox.TM.	
DS	Plasmid pPhox.TM; eukaryotic expression vector; transfected cell;	
KW	single chain antibody; sfv; molecular hook; ds.	
XX	Cytomegalovirus.	
OS	unidentified bacteriophage; T7.	
OS	Mus; sp.	
OS	influenza virus; .	
OS	Bos; taurus.	
OS	Homo; sapiens.	
OS	Escherichia; coli.	
OS	unidentified bacteriophage; SP6.	
OS	Synthetic.	
OS	Chimeric.	
XX	Key	
FT	promoter	Location/Qualifiers
FT		1..596
FT		/*tag= a
FT		/note= "cytomegalovirus immediate early promoter permits high level expression of the sfv in eukaryotic cells"
FT	promoter	638..657
FT		/*tag= b
FT		/note= "T7 promoter"
FT	CDS	737..1795
FT		/*tag= c
FT		737..799
FT	sig_peptide	/*tag= d
FT		/note= "murine Ig kappa-chain V-J2-C signal peptide directs the sfv to the plasma membrane for extracellular display"
FT	mRNA	800..826
FT		/*tag= e
FT		/product= "haemagglutinin A epitope tag"
FT		/note= "allows detection of the sfv by Mab 12CA5"
FT	mRNA	842..1555
FT		/*tag= f
FT		/product= "phox sfv"
FT		/note= "phox sfv single chain antibody recognises the happen phox and allows isolation or detection of cells displaying this sfv"
FT	mRNA	1568..1600
FT		/*tag= g
FT		/product= "Myc.1 epitope 1"
FT		/note= "allows detection of sfv by Mab 9E10.2"
FT	mRNA	1613..1645
FT		/*tag= h
FT		/product= "myc.1 epitope 2"
FT		/note= "allows detection of sfv by Mab 9E10.2"
FT	mRNA	1646..1795
FT		/*tag= i
FT		/product= "PDGFR transmembrane domain"
FT		/note= "fusion of platelet derived growth factor receptor transmembrane domain to sfv anchors the antibody to the plasma membrane for display"
FT	promoter	1831..1848
FT		/*tag= j
FT		/note= "SP6 promoter"
FT	polya_signal	1853..2081
FT		/*tag= k
FT		/note= "bovine growth hormone polyA signal permits proper processing and polyadenylation of the mRNA for stabilisation of the message"
FT	misc_feature	2212..2795
FT		/*tag= l
FT		/function= "Col E1 origin"
FT		/note= "Col E1 origin allows high copy replication and growth in E. coli"
FT	polya_signal	complement(2980)..3251
FT		/*tag= o
FT		/note= "thymidine kinase polyA site"

```

FT CDS complement(3426..4214)
FT /tag= n
FT /note= "neomycin/kanamycin resistance gene allows
FT selection of the plasmid in E. coli and confers G418
FT resistance to mammalian cells"
FT promoter complement(4249..4587)
FT /tag= m
FT /function= "SV40 origin and promoter"
FT CDS complement(4666..5526)
FT /tag= p
FT /note= "ampicillin resistance gene allows selection of
FT the plasmid in E. coli"
FT misc_feature 5557..6113
FT /tag= q
FT /function= "f1 origin"

MO9708186-A1.
06-MAR-1997.
23-AUG-1996; 96WO-US015819.
24-AUG-1995; 95US-00518835.
(INVI-) INVTITROGEN CORP.
Cheanut RD, Baytan A, Hoefler JP, Bernhard A, Chang M;
WPI; 1997-179169/16.
Eukaryotic expression vector - for identification and separation of
transfected cells from total cell population.
Example 1; Fig 6; 83pp; English.

Eukaryotic expression vector plasmid pPhox-TM (PAT63235) can be used in a
novel system for isolating and identifying transfected eukaryotic cells.
It employs a single chain antibody (scFv) directed against a hapten, phox,
to isolate transiently transfected cells from total populations in
culture. The expressed fusion protein, phox scFv, also contains 2 epitope
tag peptides and the transmembrane domain (TM) of human platelet derived
growth factor receptor (PDGFR). When expressed in transfected cells, the
fusion protein is anchored to the membrane via the PDGFR-TM, and the
antibody binding unit, phox scFv, is exposed to the extracellular
environment. The transfected cells are selected using antigen (phox)-
coated magnetic beads. The method allows for identification and selection
of transfected cells as early as 2 hr after transfection, thus allowing
study of the acute effects of the expression of the gene of interest.
(CC Updated on 27-AUG-2003 to correct OS field.)
CC
CC
CC Sequence 6115 BP; 1440 A; 1607 C; 1599 G; 1467 T; 0 U; 2 Other;
XX
XX
SQ
Query Match 98.3%; Score 934.4; DB 2; Length 6115;
Best Local Similarity 99.4%; Pred. No. 5.5e-238;
Matches 948; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 1 ATGCCGAGGTCAAGCTGCAGAGTCAAGGAGGAGCTTATGTCAGCTGAGAGGTCGCCG 60
DB 842 ATGCCGAGGTCAAGCTGCAGAGTCAAGGAGGAGCTTATGTCAGCTGAGAGGTCGCCG 901
QY 61 AAACCTCTCTGTCAGACCTCTGATTCACCTTCAGTAGCTTTGGAATGACAGTGGTTCGT 120
DB 902 AAACCTCTCTGTCAGACCTCTGATTCACCTTCAGTAGCTTTGGAATGACAGTGGTTCGT 961
QY 121 CAGGCTCCAGAGAGGGCTGAGTGGTGGCATATATTAGTAGTGGCAGTAGTACCATC 180
DB 962 CAGGCTCCAGAGAGGGCTGAGTGGTGGCATATATTAGTAGTGGCAGTAGTACCATC 1021
QY 181 TACTATGACAGACAGATGAAGGAGCATTACCATCTCCAGAGACAAATCCCAAGAACCC 240
DB 1022 TACTATGACAGACAGATGAAGGAGCATTACCATCTCCAGAGACAAATCCCAAGAACCC 1081
QY 241 CTGTTCTGCAATATGACCACTAGCTGAGGAGACAGGTATGATTATCTGTGCAAGA 300

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DB 1082 CTGTTCTGCAATATGACCACTAGCTGAGGACAGGACATGATTATTACTGTCAAGA 1141
QY 301 GATTACGGGGCTTATTTGGGGCCAAAGGACCAAGGTCACCGTCTCTCAGTGGAGGCGC 360
DB 1142 GATTACGGGGCTTATTTGGGGCCAAAGGACCAAGGTCACCGTCTCTCAGTGGAGGCGC 1201
QY 361 TCAGGCGAGAGTGCTCTGGCGGTGGCGAGATCGACATTAGCTCACCGAGTCTTCAGCA 420
DB 1202 TCAGGCGAGAGTGCTCTGGCGGTGGCGAGATCGACATTAGCTCACCGAGTCTTCAGCA 1261
QY 421 ATCATGTCGATCTCCAGGGGAGAGGTTCAACATGACTGAGTCCAGTCAAGTGA 480
DB 1262 ATCATGTCGATCTCCAGGGGAGAGGTTCAACATGACTGAGTCCAGTCAAGTGA 1321
QY 481 AGGTACATGAAGTGGTTCCCAAGAGTCAGGACCTCCCCCAAAAGATGATTTATGAC 540
DB 1322 AGGTACATGAAGTGGTTCCCAAGAGTCAGGACCTCCCCCAAAAGATGATTTATGAC 1381
QY 541 ACATCCAAACTGTCTTCTGAGAGTCCCTGCTTCACTGAGGAGTGGTCTGGGACCTCT 600
DB 1382 ACATCCAAACTGTCTTCTGAGAGTCCCTGCTTCACTGAGGAGTGGTCTGGGACCTCT 1441
QY 601 TACTCTTCACAAATGAGAGATGAGAGCTGAAGATGCTGCCACTTACTGACAGCA 660
DB 1442 TACTCTTCACAAATGAGAGATGAGAGCTGAAGATGCTGCCACTTACTGACAGCA 1501
QY 661 TGAAGTAGTAACCCACTGACGTTCCGTGCTGGGACCAAGCTGAGAGTGAACG--GCG 717
DB 1502 TGAAGTAGTAACCCACTGACGTTCCGTGCTGGGACCAAGCTGAGAGTGAACG--GCG 1561
QY 718 GCCGCAAGCAAAATCATCTTCAGAGAGATCTGAATGGGCGCTGAGCAACAAAA 777
DB 1562 GCCGCAAGCAAAATCATCTTCAGAGAGATCTGAATGGGCGCTGAGCAACAAAA 1621
QY 778 CTCATCTCAGAGAGATCTGAATGGGCGCAAGCAAGAGATCATGCTGGG 837
DB 1622 CTCATCTCAGAGAGATCTGAATGGGCGCAAGCAAGAGATCATGCTGGG 1681
QY 838 CCACACTCTTGGCCCTTTAAGGTGGTGAATTCAGCCATCTGGCCCTGGTGGTCTC 897
DB 1682 CCACACTCTTGGCCCTTTAAGGTGGTGAATTCAGCCATCTGGCCCTGGTGGTCTC 1741
QY 898 ACCATCATCTCTCTTATCATCTCTCATCATGCTTTGGCAGAGAACCAAGCTTAA 951
DB 1742 ACCATCATCTCTCTTATCATCTCTCATCATGCTTTGGCAGAGAACCAAGCTTAA 1795

RESULT 4
AAC66074
ID AAC66074 standard; DNA; 1256 BP.
XX
AC AAC66074;
XX
AC 22-FEB-2001 (first entry)
XX
DB E. coli expression plasmid pUBS520-ScFvOx DNA.
XX
KW Eukaryotic protein; protease; interferon; antibody; hormone;
XX disulfide bridge; de.
XX Escherichia coli.
XX Synthetic.
XX
PN EP1048732-A1.
XX
PD 02-NOV-2000.
XX
XX 26-APR-1999; 99BP-00107412.
XX
PF 26-APR-1999; 99BP-00107412.
XX
PR 26-APR-1999; 99BP-00107412.
XX
PA (HOPF ) HOPFMANN LA ROCHE & CO AG F.

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XX MPI; 2000-674185/66.  
 DR P-PSDB; AAB11398.  
 XX  
 XX Preparation of water-soluble eukaryotic polypeptides with disulfide  
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the  
 PT presence of arginine or amide compound.  
 XX  
 XX Example 6; Page 20-22; 40pp; German.

CC This invention describes a novel preparation of a water-soluble,  
 CC naturally occurring eukaryotic polypeptide containing two or more  
 CC cysteine units bound via a disulfide bridge which comprises cultivation  
 CC of prokaryotic cells in the presence of arginine or an amide compound.  
 CC The method is useful for the preparation of eukaryotic proteins e.g.  
 CC proteases, interferons, protein hormones, antibodies or antibody  
 CC fragments (e.g. a single chain FV fragment that binds to thyroid  
 CC stimulating hormone). It is especially useful for preparing proteins with  
 CC more than five disulfide bridges, e.g. recombinant plasminogen activator  
 CC (rPA). The technique is simple and does not require in vitro after-  
 CC treatment, such as the removal of inclusion bodies, reduction or  
 CC naturalization.

SQ Sequence 1256 BP; 304 A; 320 C; 339 G; 293 T; 0 U; 0 Other;

Query Match 78.8%; Score 749.6; DB 3; Length 1256;

Best Local Similarity 98.2%; Pred. No. 4.8e-189;

Matches 758; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGGCCGAGGTCAAGTGCAGAGTCAAGGAGGCTTAGTGAGGCTTGAGGCTCCCG 60  
 DB 199 ATGGCCGAGGTCAAGTGCAGAGTCTGGGGGAGGCTTAGTGAGGCTTGAGGCTCCCG 258  
 QY 61 AAACCTCTCTGTCGACCTCTGATTCACCTTCAGTACCTTCGAAATGACCTGGTTCGT 120  
 DB 259 AAACCTCTCTGTCGACCTCTGATTCACCTTCAGTACCTTCGAAATGACCTGGTTCGT 318  
 QY 121 CAGGCTCCAGAGAGGGGCTGAGTGGTTCGATATATTAGTAGGAGTAGTACATC 180  
 DB 319 CAGGCTCCAGAGAGGGGCTGAGTGGTTCGATATATTAGTAGGAGTAGTACATC 378  
 QY 181 TACTATGACAGACAGTGAAGGAGCATTACCATCTCCAGAGCAATCCAGAAACCC 240  
 DB 379 TACTATGACAGACAGTGAAGGAGCATTACCATCTCCAGAGCAATCCAGAAACCC 438  
 QY 241 CTGTTCTCTCAATGACAGTCTTAAGTCTGAGAGACCGGTCTATATTACTGTGAAGA 300  
 DB 439 CTGTTCTCTCAATGACAGTCTTAAGTCTGAGAGACCGGTCTATATTACTGTGAAGA 498  
 QY 301 GATTACGGGGCTTAATGGGGCCAAAGGAGCAACCGGTCTCTCAGGTGAGGCGGC 360  
 DB 499 GATTACGGGGCTTAATGGGGCCAAAGGAGCAACCGGTCTCTCAGGTGAGGCGGC 558  
 QY 361 TCAGGGGAGAGTGGCTCTGGCGGTGGCGGATTCGAGATTCAGTCCAGCA 420  
 DB 559 TCAGGGGAGAGTGGCTCTGGCGGTGGCGGATTCGAGATTCAGTCCAGCA 618  
 QY 421 ATCATGTCTGCACTCTCAAGGGAGAGGGTCAACATGACCTGCGAGTCCAGTTCAAGTGA 480  
 DB 619 ATCATGTCTGCACTCTCAAGGGAGAGGGTCAACATGACCTGCGAGTCCAGTTCAAGTGA 678  
 QY 481 AGGTACATGAATGTTCCAAAGAGTACAGGACCTCCCAAAAGATGGATTATGAC 540  
 DB 679 AGGTACATGAATGTTCCAAAGAGTACAGGACCTCCCAAAAGATGGATTATGAC 738  
 QY 541 ACATCCAAATGTTCTTCTGGAGTCCCTGCTGCTTCAATGAGGAGTCTGGAGCTCT 600  
 DB 739 ACATCCAAATGTTCTTCTGGAGTCCCTGCTGCTTCAATGAGGAGTCTGGAGCTCT 798  
 QY 601 TACTCTCTCAATGACAGAGTGAAGGCTGAAAGATGCTGCCATTACTGCGCAGAG 660  
 DB 799 TACTCTCTCAATGACAGAGTGAAGGCTGAAAGATGCTGCCATTACTGCGCAGAG 858

QY 661 TGGAGTAGTAACCACTCACTGCTGGTGTGGAGCCAAAGCTGAGTGAAGCGGCGCC 720  
 DB 859 TGGAGTAGTAATCACTCACTTCCGTTGGGAGCCAAAGCTGAGTGAAGCGGCGCC 918  
 QY 721 GCAGAACAAAATCTATCTCAGAGAGATCTGAATGGGGCGCTCCAGCAAC 772  
 DB 919 GCAGAACAAAATCTATCTCAGAGAGATCTGAATGGGGCGCTCCAGTATAC 970

# RESULT 5

AAE77806  
 ID AAE77806 standard; DNA; 1256 BP.

AC AAE77806;

DT 29-MAY-2001 (first entry)

DE Fragment of PUBS520-ScFvOX coding for Pe1B-ScFvOXazolon fusion protein.

KW Molecular chaperrone; Pe1B signal sequence; scFvOXazolon; ds.

XX Unidentified.

PN EP1077262-A1.

PD 21-FEB-2001.

PF 24-JUL-2000; 2000EP-00115839.

PR 29-JUL-1999; 99EP-00114811.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;

DR MPI; 2001-246712/26.

PT P-PSDB; AAB74199.

PT Producing naturally folded eukaryotic proteins e.g. antibodies,

PT interferon, hormones or proteases that contain two or several cysteines

PT linked by disulfide bridges comprises co-expression of a molecular

PS chaperrone.

XX Example 6; Page 17-18; 35pp; English.

CC The present invention relates to a method for production of a naturally

CC folded eukaryotic protein containing two or more cysteines linked by

CC disulfide bridges. The method comprises co-expression and secretion into

CC the periplasm of a molecular chaperrone via an expression vector coding

CC for the chaperrone. The expression vector also encodes a signal sequence.

CC The method is useful for producing a naturally folded eukaryotic protein

CC such as an antibody, antibody fragment, interferon, protein hormone or a

CC protease containing two or several cysteines linked by disulfide bridges.

CC The present sequence is a fragment of expression vector PUBS520-ScFvOX,

CC which codes for a fusion protein composed of the Pe1B signal sequence and

CC ScFvOXazolon. This sequence was used in the method of the present

SQ Sequence 1256 BP; 304 A; 321 C; 339 G; 292 T; 0 U; 0 Other;

Query Match 78.8%; Score 749.6; DB 4; Length 1256;

Best Local Similarity 98.2%; Pred. No. 4.8e-189;

Matches 758; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 ATGGCCGAGGTCAAGTGCAGAGTCAAGGAGGCTTAGTGAGGCTTGAGGCTCCCG 60  
 DB 199 ATGGCCGAGGTCAAGTGCAGAGTCTGGGGGAGGCTTAGTGAGGCTTGAGGCTCCCG 258  
 QY 61 AAACCTCTCTGTCGACCTCTGATTCACCTTCAGTACCTTCGAAATGACCTGGTTCGT 120  
 DB 259 AAACCTCTCTGTCGACCTCTGATTCACCTTCAGTACCTTCGAAATGACCTGGTTCGT 318  
 QY 121 CAGGCTCCAGAGAGGGGCTGAGTGGTTCGATATATTAGTAGGAGTAGTACATC 180

Db 319 CAGGCTCCAGAGAGGGCTGAGTGGTGCATATATTAGTAGGCGATGTACCATC 378  
 Oy 181 TACTATGACAGACAGTGAAGGAGACGATTCACCATCTCCAGAGACAAATCCCAAGAACCC 240  
 Db 379 TACTATGACAGACAGTGAAGGAGACGATTCACCATCTCCAGAGACAAATCCCAAGAACCC 438  
 Oy 241 CTGTTCTTCGCAAAATGACAGTCTTAAGTCTGAGAGACAGCGTCAATGATTACTGTGCAGAA 300  
 Db 439 CTGTTCTTCGCAAAATGACAGTCTTAAGTCTGAGAGACAGCGCATGATTAATGCGCAGAA 498  
 Oy 301 GATTACGGGGCTTATTTGGGGCCCAAGGAGACAGGTCACCGCTTCTCCAGTGTGAAGCGGC 360  
 Db 499 GATTACGGGGCTTATTTGGGGCCCAAGGAGACAGGTCACCGCTTCTCCAGTGTGAAGCGGT 558  
 Oy 361 TCAGGCGGAGGTGGCTCTTGGCGGTGGCGGATGCGACATGAGCTCAACCCAGTCTCCAGCA 420  
 Db 559 TCAGGCGGAGGTGGCTCTTGGCGGTGGCGGATGCGACATGAGCTCAACCCAGTCTCCAGCA 618  
 Oy 421 ATCATGTCTGCATCTTCAGAGGAGAGGATCACCATGACCTGCAAGTCCAGTCAAGTGA 480  
 Db 619 ATCATGTCTGCATCTTCAGAGGAGAGGATCACCATGACCTGCAAGTCCAGTCAAGTGA 678  
 Oy 481 AGGTACATGAATGTGTTCCAAAGATGACGACCTCCCAAAAGATGATTTATGAC 540  
 Db 679 AGGTACATGAATGTGTTCCAAAGATGACGACCTCCCAAAAGATGATTTATGAC 738  
 Oy 541 ACATCCAAACTGCTCTTCTGAGATCCCTGCTCCCTTCAGTGGAGTGGGTCTGGACCTCT 600  
 Db 739 ACATCCAAACTGCTCTTCTGAGATCCCTGCTCCCTTCAGTGGAGTGGGTCTGGACCTCT 798  
 Oy 601 TACTCTTCACATGACAGCATGAGAGGCTGAAGATGCTGCACTTAATCTGCCAGCAG 660  
 Db 799 TACTCTTCACATGACAGCATGAGAGGCTGAAGATGCTGCACTTAATCTGCCAGCAG 858  
 Oy 661 TGGAGTAGTAACCACTACGTTGGTGGTGGAGCCAAAGCTGAGAGTGAAGGGCGGCGC 720  
 Db 859 TGGAGTAGTAACCACTACGTTGGTGGTGGAGCCAAAGCTGAGAGTGAAGGGCGGCGC 918  
 Oy 721 GCAGAACAAAATCTCATCTCAGAGAGGATCTGAATGGGGCCGTGACGAGAC 772  
 Db 919 GCAGAACAAAATCTCATCTCAGAGAGGATCTGAATGGGGCCGTGATGTAAC 970

RESULT 6  
 AAF61193  
 ID AAF61193 standard; DNA; 1256 BP.  
 XX AAF61193;  
 AC AAF61193;  
 XX  
 DT 18-MAY-2001 (first entry)  
 XX  
 DE Expression plasmid pUBS520-ScFvOx DNA.  
 XX  
 KM Chaperone protein; periplasm; antibody production; protein production;  
 KM interferon production; protease production; ds.  
 XX  
 OS Escherichia coli.  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT CDS 199..966  
 FT /\*tag= a  
 FT /product= "pUBS520-ScFvOx"  
 PN EP1077263-A1.  
 PD 21-FEB-2001.  
 XX  
 PF 29-JUL-1999; 99EP-00114811.  
 XX  
 PR 29-JUL-1999; 99EP-00114811.  
 XX

PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 XX WPI; 2001-204356/21.  
 DR P-PSDB; AAB70769.  
 XX  
 PT Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by  
 PT simultaneous expression of a chaperone protein, allows simple recovery  
 PT from periplasm or medium.  
 XX  
 PS Example 6; Page 18-20; 36pp; German.  
 XX  
 CC This invention describes a novel method for preparing a naturally folded  
 CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged  
 CC Cys residues by culturing prokaryotic cells that contain an expression  
 CC vector for (I) including a prokaryotic signal sequence at its N-terminus  
 CC and a nucleic acid (II) that secretes a chaperone protein (III) into the  
 CC periplasm. (I) is secreted into the periplasm or medium; the signal  
 CC peptide is then cleaved and (I) isolated from the periplasm or medium.  
 CC The method is used for production of antibody, interferon, protein  
 CC hormone or protease. Expression of (III) increases the yield of (I). The  
 CC method is simple and eliminates time-consuming in vitro processing  
 CC operations such as dissolution of inclusion bodies, reduction and  
 CC refolding. (III) protects (I) against agglomeration and promotes their  
 CC natural conformation  
 CC  
 XX Sequence 1256 BP; 304 A; 320 C; 339 G; 293 T; 0 U; 0 Other;  
 XX  
 SQ  
 Query Match 78.8%; Score 749.6; DB 4; Length 1256;  
 Best Local Similarity 98.2%; Pred. No. 4,8e-189;  
 Matches 758; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 1 ATGCGCAGAGTCAAGCTTCAGAGAGTCAAGGAGGCTTATGACAGCTTCGAGGCTCCCGG 60  
 Db 199 ATGCGCAGAGTCAAGCTTCAGAGAGTCAAGGAGGCTTATGACAGCTTCGAGGCTCCCGG 258  
 Oy 61 AAACCTCTCTGCGAGCCTCTGAGATTCCTTCACTTCACTTGAATGACATGGGTTCGT 120  
 Db 259 AAACCTCTCTGCGAGCCTCTGAGATTCCTTCACTTCACTTGAATGACATGGGTTCGT 318  
 Oy 121 CAGGCTCCAGAGAGGAGGCTGAGTGGTGGTCCATATATAGTGGAGTGTATCATC 180  
 Db 319 CAGGCTCCAGAGAGGAGGCTGAGTGGTGGTCCATATATAGTGGAGTGTATCATC 378  
 Oy 181 TACTATGACAGACAGTGAAGGAGATTCACCATCTCCAGAGACAAATCCCAAGAACCC 240  
 Db 379 TACTATGACAGACAGTGAAGGAGCCGATTCACCATCTCCAGAGACAAATCCCAAGAACCC 438  
 Oy 241 CTGTTCTTCGCAAAATGACAGTCTTAAGTCTGAGAGACAGCGTCAATGATTACTGTGCAGAA 300  
 Db 439 CTGTTCTTCGCAAAATGACAGTCTTAAGTCTGAGAGACAGCGCTATGATTAATGCGCAGAA 498  
 Oy 301 GATTACGGGGCTTATTTGGGGCCCAAGGAGACAGGTCACCGCTTCTCCAGTGTGAAGCGGC 360  
 Db 499 GATTACGGGGCTTATTTGGGGCCCAAGGAGACAGGTCACCGCTTCTCCAGTGTGAAGCGGT 558  
 Oy 361 TCAGGCGGAGGTGGCTCTTGGCGGTGGCGGATGCGACATGAGCTCAACCCAGTCTCCAGCA 420  
 Db 559 TCAGGCGGAGGTGGCTCTTGGCGGTGGCGGATGCGACATGAGCTCAACCCAGTCTCCAGCA 618  
 Oy 421 ATCATGTCTGCATCTTCAGAGGAGAGGATCACCATGACCTGCAAGTCCAGTCAAGTGA 480  
 Db 619 ATCATGTCTGCATCTTCAGAGGAGAGGATCACCATGACCTGCAAGTCCAGTCAAGTGA 678  
 Oy 481 AGGTACATGAATGTGTTCCAAAGATGACGACCTCCCAAAAGATGATTTATGAC 540  
 Db 679 AGGTACATGAATGTGTTCCAAAGATGACGACCTCCCAAAAGATGATTTATGAC 738  
 Oy 541 ACATCCAAACTGCTCTTCTGAGATCCCTGCTCCCTTCAGTGGAGTGGGTCTGGACCTCT 600  
 Db 739 ACATCCAAACTGCTCTTCTGAGATCCCTGCTCCCTTCAGTGGAGTGGGTCTGGACCTCT 798  
 Oy 601 TACTCTTCACATGACAGCATGAGAGGCTGAAGATGCTGCACTTAATCTGCCAGCAG 660

Db	799	TACTCTGCACATCAGCAGCATGGAGGCTGAAGTCTGCCACTTATTACTGCACAG	857
Qy	661	TGAGTAGTAAACCATCTCACTGTTCCGTGTGGGACCAAGCTGAGAGCTGAACCGGCGGCC	720
Db	859	TGAGTAGTAAATTCCTCACTTCCTCGGTGCTGGGACCAAGCTGAGAGCTGAACCGGCGGCC	918
Qy	721	GCAGAACAAAACTCATCTCAGAGGAGATCGAATGGGGCGTCGACGAAC	772
Db	919	GCAGAACAAAACTCATCTCAGAGGAGATCGAATGGGGCGCATGATTAAC	970
RESULT 7			
ID	AAD02212	AAD02212 standard; DNA; 1256 BP.	
AC	AAD02212;		
XX	28-MAR-2001	(first entry)	
DT	Partial	PUBS520-pIN-scfVox encoding PelB-scfVoxazolon fusion protein.	
XX	Secreted protein; plasmid	PUBS520-pIN-scfVox; chaparone; interferon;	
KW	protease; hormone; naturally folded protein; fusion protein; DnaJ;		
KM	heat shock protein; HSP; peptidase lyase B; PelB; hapten; lac promoter;		
KM	single-chain Fv-fragment Oxazolon; scfVoxazolon;		
KW	thyroid stimulating hormone; TSH; db.		
XX	Pectobacterium carotovorum.		
OS	Escherichia coli.		
OS	Unidentified.		
OS	Chimeric.		
XX	Key	Location/Qualifiers	
FH	CDS	199..966	
FT	/*tag= a	/product= "Erwinia carotovora PelB signal sequence-	
FT	single-chain Fv-fragment Oxazolon fusion protein"		
FT	/note= "CDS has an additional stop codon at position 967-		
FT	969"		
XX	EP1054063-A2.		
PD	22-NOV-2000.		
XX	19-APR-2000; 2000EP-00108505.		
XX	26-APR-1999; 99EP-00107412.		
XX	(HOFF ) HOFFMANN LA ROCHE & CO AG F.		
PA	Ambrosius D, Rudolph R, Schaeffner J, Schwarz B;		
XX	WPI; 2001-033777/05.		
PI	P-PsDB; AAY72020.		
XX	Producing water-soluble, naturally folded, and secreted eukaryotic		
PT	polypeptide, involves culturing prokaryotic cells containing an		
PT	expression vector encoding the polypeptide in the presence of arginine or		
PT	a specific compound.		
XX	Example 6; Page 20-22; 35pp; English.		
XX	The patent discloses a method for the production of a water-soluble,		
CC	naturally folded and secreted eukaryotic proteins in prokaryotic cells.		
CC	The method involves culturing the prokaryotic cells, containing an		
CC	expression vector encoding the desired protein and the prokaryotic signal		
CC	sequence, in the presence of an additive, e.g., L-arginine. The signal		
CC	sequence mediates the secretion of the desired protein into the		
CC	periplasm, where folding of the protein takes place. The prokaryotic cell		
CC	also contains an expression vector encoding a molecular chaperone, e.g.,		
CC	DnaJ and heat shock protein 25 (HSP25). The simultaneous co-		
CC	overexpression and co-secretion of molecular chaperones in the periplasm		
CC	improves the yield of functionally folded protein. The above method		

	recombinantly produces a high yield of eukaryotic secreted proteins in prokaryotes. The method is useful for producing eukaryotic proteins such as an antibody, antibody fragment, interferon, protein hormone or a protease. The present sequence is a part of an expression plasmid, pUBS520-PIN-scFvOX, which comprises the lac promoter, the Ewhita carotovora pectate lyase B (PelB) signal sequence and the scfVox gene. The single-chain Fv-fragment, which is directed against the hapten oxazolin (ScfvOxazolin), is an antibody fragment against thyroid stimulating hormone (TSH). The co-expression of ScfvOX which has no chaperrone properties is used as a negative control
XX	Sequence 1256 BP; 304 A; 320 C; 339 G; 293 T; 0 U; 0 Other;
SQ	
Query Match	78.8%; Score 749.6; DB 5; Length 1256;
Best Local Similarity	98.2%; Pred. No. 4.8e-189;
Matches 758; Conservative	0; Mismatches 14; Indels 0; Gaps 0.
Dy	1 ATGGCCGAGGTCAAGCTGCAGAGTCAAGGGGAGGCTTAGTCAGACCTCGAGGGTCCGG 60
Dy	199 ATGGCCGAGGTCAAGCTGCAGAGTCTGGGGAGGCTTAGTCAGACCTCGAGGGTCCGG 258
Dy	61 AAATCTCTCTGTGACGCTCTGGAATCACTTTCAGTAGTGATGATGACCTGGGTTCTG 120
Dy	259 AAATCTCTCTGTGACGCTCTGGAATCACTTTCAGTAGTGATGATGACCTGGGTTCTG 318
Dy	121 CAGGCTTCAAGAAAGGGGCTGGAATGGGTGCAATATTAGTAGTGAGTAATCATC 180
Dy	319 CAGGCTTCAAGAAAGGGGCTGGAATGGGTGCAATATTAGTAGTGAGTAATCATC 378
Dy	181 TACTATGCAGACAGTGAAGGAGCAATTCACATCTCCAGAACAATCCCAAGAACACC 240
Dy	379 TACTATGCAGACAGTGAAGGAGCAATTCACATCTCCAGAACAATCCCAAGAACACC 438
Dy	241 CTGTTCTGTCAAAATGACAGCTTAGAGTCTGAGGACACGCTCATGTATTACTGTGACA 300
Dy	439 CTGTTCTGTCAAAATGACAGCTTAGAGTCTGAGGACACGCTCATGTATTACTGTGACA 498
Dy	301 GATTACGGGGCTTATTGGGGCCAAAGGACACACGCTCACCGTCTCTCAGGTGAGGCCGC 360
Dy	499 GATTACGGGGCTTATTGGGGCCAAAGGACACACGCTCACCGTCTCTCAGGTGAGGCCGC 558
Dy	361 TCAGGCGGAGGTGGCTCTGGCGGCTGGGGGATCGGACATTGAGCTCACCCAGTCTCCAGA 420
Dy	559 TCAGGCGGAGGTGGCTCTGGCGGCTGGGGGATCGGACATTGAGCTCACCCAGTCTCCAGA 618
Dy	421 ATCATGTCTGATCTCCAGGGGAGAGGGTCAACATGACCTGACAGTGCAGTTCAAATGTA 480
Dy	619 ATCATGTCTGATCTCCAGGGGAGAGGGTCAACATGACCTGACAGTGCAGTTCAAATGTA 678
Dy	481 AGGTACATGAATCTGGTTCACAGAGTCAGGACCTTCCCCAAGAATGATTTATGAC 540
Dy	679 AGGTACATGAATCTGGTTCACAGAGTCAGGACCTTCCCCAAGAATGATTTATGAC 738
Dy	541 ACATCCAAACGTCTTCTGGAGTCCCGTCCGCTTCAAGTGGCAATGGGCTCGGGACCTCT 600
Dy	739 ACATCCAAACGTCTTCTGGAGTCCCGTCCGCTTCAAGTGGCAATGGGCTCGGGACCTCT 798
Dy	601 TACTCTTCACAATCAGCAGCATGAGGCTGAGATGCTGCACCTTACTACTGCCCAGAG 660
Dy	799 TACTCTTCACAATCAGCAGCATGAGGCTGAGATGCTGCACCTTACTACTGCCCAGAG 858
Dy	661 TGAGTAGTAAACCACTCAAGTTCGGTCTGGGACCAAGCTGAGCTGAAAACGGCGGCC 720
Dy	859 TGAGTAGTAAACCACTCAAGTTCGGTCTGGGACCAAGCTGAGCTGAAAACGGCGGCC 918
Dy	721 GCAGAAACAAAACTCATCTCAGAAAGAGATCTGAATGGGGCCGTCGAGCAAC 772
Dy	919 GCAGAAACAAAACTCATCTCAGAAAGAGATCTGAATGGGGCCGTCGAGCAAC 970

```
XX AC AC84876;
XX
XX 03-OCT-2003 (first entry)
XX
XX Single-chain (scFv) antibody encoding DNA.
XX
XX Transgenic; biomolecule; ATP; ADP; cytoskeletal; virucide; gene therapy;
XX antisense therapy; scFv; gene; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 67..789
XX FT /tag= a
XX FT /product= "scFv antibody"
XX
XX EP121524-A1.
XX
XX 25-JUN-2003.
XX
XX 19-DEC-2001; 2001EP-00130319.
XX
XX 19-DEC-2001; 2001EP-00130319.
XX
XX (DUEB/) DUEBING K.
XX
XX Mahn A, Hanke S, Petach D;
XX
XX WPI: 2003-543829/52.
XX
XX P-PSDB; ABR62010.
XX
XX
XX Increasing the content of transgene-coded biomolecules in a plant or
XX animal, useful for producing proteins for diagnosing, preventing and/or
XX treating viral diseases and cancer, comprises changing the distribution
XX of ATP and/or ADP.
XX
XX Example 2, Fig 2, 18pp; English.
XX
XX The invention relates to increasing the content of one or more transgene-
XX coded biomolecules in an organism and involves changing the distribution
XX of ATP and/or ADP in cells of the organism. The yield of transgenic
XX molecules in host cells is often insufficient for industrial production.
XX The method increases the yield of transgenic molecules in animal and
XX plant host cells, therefore facilitating their production on an
XX industrial scale. The proteins produced by the method are useful for
XX diagnosing, preventing and/or treating viral diseases and cancer. The
XX present sequence represents a DNA encoding a single-chain (scFv)
XX antibody, used to exemplify the increase in the expression of scFv
XX antibodies in transgenic potato tubers
XX
XX Sequence 843 BP; 200 A; 214 C; 230 G; 199 T; 0 U; 0 Other;
XX
XX Query Match 77.5%; Score 737; DB 9; Length 843;
XX Best Local Similarity 97.4%; Pred. No. 9, 4e-186;
XX Matches 749; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
XX
XX 4 GCCGAGTCAGAGCTCAGAGTCAGAGGAGGCTTAGTGACAGCTGAGAGTCCCGAAA 63
XX 70 GGTATGTGACAGCTGTGAGTCTGGGGAGGCTTAGTGACAGCTGAGAGTCCCGAAA 129
XX
XX 64 CTCTCTGTGACAGCTCTGTGATTCAGTTCACTTGAATGCACTGAGTGTCTGAC 123
XX 130 CTCTCTGTGACAGCTCTGTGATTCAGTTCACTTGAATGCACTGAGTGTCTGAC 189
XX
XX 124 GGTCCAGAGAGGGCTGAGTGGTCCGATATATTAGTAGGAGAGTACCATCTAC 183
XX 130 GGTCCAGAGAGGGCTGAGTGGTCCGATATATTAGTAGGAGAGTACCATCTAC 249
XX
XX 184 TATGAGACACAGTAAAGGAGCATTCACATCTCAGAGACATCCCAAGAACCCCTG 243
XX 250 TATGAGACACAGTAAAGGAGCATTCACATCTCAGAGACATCCCAAGAACCCCTG 309
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```
QY 244 TTCTTGCAATGACCAAGCTTAAAGCTTGAAGACACAGCTCATGTATTACTGTGCAAGAGAT 303
DB 310 TTCTTGCAATGACCAAGCTTAAAGCTTGAAGACACAGGCTCATGTATTACTGTGCAAGAGAT 369
QY 304 TACGGGAGCTTATTGGGGGCAAGGAGCAACGGTCACTGCTCCTGAGTGGAGCGGCTCA 363
DB 370 TACGGGAGCTTATTGGGGGCAAGGAGCAACGGTCACTGCTCCTGAGTGGAGCGGCTCA 429
QY 364 GCGGAGGTGAGCTGTGGGCGGTGGCGGATCGGACATTGAGCTTACCCAGTCTTCAGCAATC 423
DB 430 GCGGAGGTGAGCTGTGGGCGGTGGCGGATCGGACATTGAGCTTACCCAGTCTTCAGCAATC 489
QY 424 ATGTCTGATCTCCAGGGGAGAGGATCAACATGACCTGAGTGGCAAGTTCAAGTAAAG 483
DB 430 ATGTCTGATCTCCAGGGGAGAGGATCAACATGACCTGAGTGGCAAGTAAAG 549
QY 484 TACATGAAGCTGTTCCAGACAGAGTCAAGGACAGCTCCCGCAAAAGATGATTATATACACA 543
DB 550 TACATGAAGCTGTTCCAGACAGAGTCAAGGACAGCTCCCGCAAAAGATGATTATATACACA 609
QY 544 TCCAAACTGTCTTGTGAGTCCCTGCTGCTTCACTGAGTGGAGTGTGGACCTTTAC 603
DB 610 TCCAAACTGTCTTGTGAGTCCCTGCTGCTTCACTGAGTGGAGTGTGGACCTTTAC 669
QY 604 TCTTCACATCAGAGATGAGGCTGAAGATGCTGCCACTTACTTCCAGCAGTGG 663
DB 670 TCTTCACATCAGAGATGAGGCTGAAGATGCTGCCACTTACTTCCAGCAGTGG 729
QY 664 AGTAGTAAACCACTCAGCTTGGTGGTGGAGCCAACTGAGAGTGAACCGGCGGCGCA 723
DB 730 AGTAGTAAACCACTCAGCTTGGTGGTGGAGCCAACTGAGAGTGAACCGGCGGCGCA 789
QY 724 GAACAAATCATCTCAGAAAGAGATCTGAATGAGGCGCTGACGAAC 772
DB 790 GAACAAATCATCTCAGAAAGAGATCTGAATGAGTCAAAAGAGAAC 838

RESULT 9
AAK98639
ID AAK98639 standard; DNA; 726 BP.
AC
XX AAK98639;
XX
XX 03-MAY-2002 (first entry)
XX
XX scFv antibody coding sequence.
XX
XX Ketone binding protein; oxazole; pathogen resistance; virucide;
XX fungicide; antibacterial; scFv antibody; gene; ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX CDS 1..726
XX FT /*tag= a
XX FT /product= "scFv antibody"
XX FT /trans_except= (pos:409..411,aa:Gly)
XX FT /trans_except= (pos:601..603,aa:Val)
XX
XX W0200204020-A2.
XX
XX 17-JAN-2002.
XX
XX 17-MAY-2001; 2001WO-DE001916.
XX
XX 12-JUL-2000; 2000DE-01033750.
XX
XX (MPBC-) MPB COLOGNE GMBH.
XX
XX Duerling K, Brinkmann O;
XX
XX WPI: 2002-154868/20.
```

DR P-PSDB, AAM48925.

XX Imparting pathogen resistance to plants and animals, comprises using a  
PT polypeptide that binds to an oxazole-derived ketone, optionally expressed  
PT from nucleic acid.

XX Example 3, Fig 1, 20pp, German.

XX The present invention relates to the use of a polypeptide that binds a  
CC ketone derived from oxazole for generating pathogen resistance in an  
CC organism. This can be used to impart resistance to pathogens (bacteria,  
CC fungi or viruses) to a wide range of plants (e.g. cereals, sugar beet,  
CC tobacco etc.), humans, farm animals and pets. Exemplified are activities  
CC against Phytophthora infestans and Erwinia carotovora in potatoes and  
CC Staphylococcus aureus in mice. The present sequence is a sc-Fv antibody  
CC coding sequence, which encodes a protein capable of binding 2-  
XX phenylloxazol-5-one

SQ Sequence 726 BP; 166 A; 184 C; 214 G; 162 T; 0 U; 0 Other;

Query Match 73.5%; Score 699.4; DB 6; Length 726;

Best Local Similarity 97.8%; Pred. No. 9e-176;

Matches 709; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 ATGGCCGAGGTCAAGCTGACAGAGTCAAGGAGGCTTATGTCAGCTTGAGGGTCCCG 60  
DB 1 ATGGCTGATGTGACGCTGGGTGAGTCTGGGGGAGGCTTATGTCAGCTTGAGGGTCCCG 60  
QY 61 AAACCTCTCTGTGACAGCTCTGATTCACCTTTCAGTATGAGTTCAGTATGAGTTCAGT 120  
DB 61 AAACCTCTCTGTGACAGCTCTGATTCACCTTTCAGTATGAGTTCAGTATGAGTTCAGT 120  
QY 121 CAGGCTCCAGAGAGGGGCTGAGTGGGTGCGATATATAGTATGAGTATGAGTATGAGTATC 180  
DB 121 CAGGCTCCAGAGAGGGGCTGAGTGGGTGCGATATATAGTATGAGTATGAGTATGAGTATC 180  
QY 181 TACTATGACAGACACAGTAAAGGAGGATTCACCATCTCCAGAGACATCCCAAGAACCC 240  
DB 181 TACTATGACAGACACAGTAAAGGAGGATTCACCATCTCCAGAGACATCCCAAGAACCC 240  
QY 241 CTGTTCTCTGCAATGACCACTTACAGTCTGAGAGACACGGTATGATTTACTGTGCAAGA 300  
DB 241 CTGTTCTCTGCAATGACCACTTACAGTCTGAGAGACACGGTATGATTTACTGTGCAAGA 300  
QY 301 GATTACGGGGCTTATTTGGGGCCAAAGGAGACCAAGGATCCGCTCTCAGGTGAGGGGGC 360  
DB 301 GATTACGGGGCTTATTTGGGGCCAAAGGAGACCAAGGATCCGCTCTCAGGTGAGGGGGC 360  
QY 361 TCAGGGGAGGTGGCTCTGGCGGTGGCGATTCGGAATGAGTCAATGAGTCCAGAGCA 420  
DB 361 TCAGGGGAGGTGGCTCTGGCGGTGGCGATTCGGAATGAGTCAATGAGTCCAGAGCA 420  
QY 421 ATCATATCTGTCATCTCCAGGGGAGAGGGTTCACATGACCTGCGAGTGCAGTTAAAGTGA 480  
DB 421 ATCATATCTGTCATCTCCAGGGGAGAGGGTTCACATGACCTGCGAGTGCAGTTAAAGTGA 480  
QY 481 AGGTACATGAACTGTTCCAAAGAGATGACGACCTCCCAAAAGATGATTTATGAC 540  
DB 481 AGGTACATGAACTGTTCCAAAGAGATGACGACCTCCCAAAAGATGATTTATGAC 540  
QY 541 ACATCCAAACGTCTTCTGGAGTCCCTGCTGCTTCAAGTGGAGTGGAGCTCT 600  
DB 541 ACATCCAAACGTCTTCTGGAGTCCCTGCTGCTTCAAGTGGAGTGGAGCTCT 600  
QY 601 TACTCTCTCAGCATCAGCAGATGAGAGGCTGAAGATGCTGCCCTTACTGTCACGACG 660  
DB 601 TACTCTCTCAGCATCAGCAGATGAGAGGCTGAAGATGCTGCCCTTACTGTCACGACG 660  
QY 661 TGGAGTAGTAACCATCTCAGCTCGGAGTGGAGACCAAGTGGAGTGAAGAGGGGGCC 720  
DB 661 TGGAGTAGTAACCATCTCAGCTCGGAGTGGAGACCAAGTGGAGTGAAGAGGGGGCC 720  
QY 721 GCAGA 725

DB 721 GCATA 725

RESULT 10

AA080468

ID AA080468 standard; DNA; 738 BP.

XX AA080468;

DT 25-MAR-2003 (revised)

DT 13-SEP-1993 (first entry)

DE Single chain antibody (scFv) which binds to phenylloxazolone.

KM Genetic selection; ligand binding protein; cholera toxin; promoter;

KM regulatory domain; lac; transmembrane domain;

XX Synthetic.

FT Key Location/Qualifiers

FT CDS 1..723

FT /tag= a /product= "single chain antibody."

DE4319296-A1.

PD 15-DEC-1994.

XX 10-JUN-1993; 93DE-04319296.

XX 10-JUN-1993; 93DE-04319296.

PA (BEHM ) BEHRINGER AG.

XX Fritz H, Hennecke F, Kolmar H;

XX WPI; 1995-023689/04.

DR P-PSDB; AAR68613.

PT Genetic selection of ligand binding proteins in microorganisms - by  
PT extracytoplasmic protein presentation, then use of ligand binding to  
PT express a detectable or selectable function.

XX Example 2.2; Fig 4; 25pp, German.

XX Genetic selection in microorganisms, for ligand binding proteins (LBP)

CC comprises: extracytoplasmic presentation of LBP and; using the signal of

CC ligand binding (by signal transduction on the biosynthetic machinery of

CC the microorganisms) to express a detectable or selectable function.

CC Microorganisms for this process include a genetically stable

CC detection/selection and are transformed with a replicon encoding a fusion

CC protein consisting of the LBP, a transmembrane helix and regulatory

CC domain. The detection/selection function is expression of a beta-

CC galactosidase gene, integrated into the chromosome and under the control

CC of the ctx (cholera toxin) promoter. The transmembrane helix is taken

CC from the toxR gene. Four primers (AA080457-60) were used in the

CC construction of the plasmid pHToxscFv. The primers described in AA080457

CC -58 were used to amplify variable heavy chain sequence of the single

CC chain antibody NQ10.12.5 and those described in AA080459-60 were used to

CC amplify the corresponding light chain sequence from the same antibody.

CC The amplified sequences were cloned into the plasmid pHToxscFv (see

CC AA080454-56 for details) to create a toxR-scFv fusion gene. This sequence

CC encodes the single chain antibody (scFv). (Updated on 25-MAR-2003 to

CC correct PN field.)

XX

SQ Sequence 738 BP; 170 A; 190 C; 209 G; 169 T; 0 U; 0 Other;

Query Match 68.9%; Score 655.4; DB 2; Length 738;

Best Local Similarity 95.0%; Pred. No. 4.6e-164;

Matches 677; Conservative 0; Mismatches 36; Indels 0; Gaps 0;





Db	1	GAAGTCAGAGCTGGATGAGTCTGGGGGAGGCTTAGTGACAGCTGAGGGGTCCCGGAAATC	60
Qy	67	TCTGTGACACCTCTGGATTTCACTTTCAGTACCTTTGGAATGCACTGGGTTCTGCAGGCT	120
Db	61	TCTGTGTGCACCTCTGGATTTCACTTTCAGTACCTTTGGAATGCACTGGGTTCTGCAGGCT	120
Qy	127	CCAGAGAAAGGGGCTGGAGTGGGTGCGCATATATTAGTAGAGGAGATGATACATCTACAT	180
Db	121	CCAGAGAAAGGGGCTGGAGTGGGTGCGCATATATTAGTAGAGGAGATGATACATCTACAT	180
Qy	187	GCAGACACAGTGAAGGAGCGATTCACCATCTCCAGAGCAATCCGAGAACCCCTGTTTC	240
Db	181	GCAGACACAGTGAAGGAGCGATTCACCATCTCCAGAGCAATCCGAGAACCCCTGTTTC	240
Qy	247	CTGCAATATGACCGATCTTAAGGTCTGAGGACAGGCTCATGTATTACTGTGCAAGATTAC	300
Db	241	CTGCAATATGACCGATCTTAAGGTCTGAGGACAGGCTCATGTATTACTGTGCAAGATTAC	300
Qy	307	GGGGCTTATTGGGGCCAGAGGACCAAGGTCACCGTCTCTAGAGTGAAGGGGCTCAGGC	360
Db	301	GGGGCTTATTGGGGCCAGAGGACCTGTGTCACTGTCTGCAAGGTGTGTGTAGCGGT	360
Qy	367	GGAGTGGCTCTGCGCGGTGGCGGATCGCATTTGAGCTCACCCAGTCTCCAGCAATCATG	420
Db	361	GGTGGGGGAGGTGGCGGCGGCTCTCAAAATGTTTCTCACCCAGTCTCCAGCAATCATG	420
Qy	427	TCTGCATCTTCAGAGGAGAGAGGTACCATATGACTGTGACAGTTCAGATGTAAAGTAC	480
Db	421	TCTGCATCTTCAGAGGAGAGAGGTACCATATGACTGTGACAGTTCAGATGTAAAGTAC	480
Qy	487	ATGAATCTGGTTCGAAGAAAGTCAAGGCACTCTCCCAAAAGATGGAATTATGACACATCC	540
Db	481	ATGAATCTGGTTCGAAGAAAGTCAAGGCACTCTCCCAAAAGATGGAATTATGACACATCC	540
Qy	547	AAACTGTCTTCTGAGTCTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCT	600
Db	541	AAACTGTCTTCTGAGTCTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCT	600
Qy	607	CTCACAATTCAGCAGCATGAGGCTGAAGATGCTGCCACTTACTGTCAGCAGTGAAGT	660
Db	601	CTCACAATTCAGCAGCATGAGGCTGAAGATGCTGCCACTTACTGTCAGCAGTGAAGT	660
Qy	667	AGTAAACCCACTCACTGTTGGTGTCTGGGACCAAGCTGAGAGCTGAACG 713	
Db	661	AGTAAATCACTCACTGTTGGTGTCTGGGACCAAGCTGAGAGCTGAACG 707	

RESULT 12

AAQ37460

ID AAQ37460 standard; DNA; 672 BP.

XX

AC AAQ37460;

XX

DT 25-MAR-2003 (revised)

DT 19-JUN-1993 (first entry)

XX

DE VH NQ10/12.5-VK NQ10/12.5 linked coding sequence.

XX

XX Primer: human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;

KM lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;

KM In-cell PCR; cloning; polymorphic; TCR V; antipeptidoxazolone; hybridoma

XX NQ2/12.4; NQ10/12.5; 86.

OS Synthetic.

OS

XX Key Location/Qualifiers

FT m18c\_RNA 1..342

FT /\*tag= a

FT /label= VH\_NQ10/12.5

FT primer\_bind 5..26

FT /\*tag= b

FT /label= NQ10/12.5\_BACK

FT primer\_bind 38..58

FT		/cag= c	/label= NO10/12.5BKRES
FT	primer_bind	complement(41. .60)	
FT		/cag= d	
FT	primer_bind	/label= NQHPRB	
FT		complement(310. .355)	
FT		/cag= e	
FT	primer_bind	/label= MOVHlink4	
FT		330. .373	
FT		/cag= h	
FT	misc_feature	/label= MOVkappalnk4	
FT		343. .348	
FT		/cag= f	
FT	misc_RNA	/note= "Linker Peptide"	
FT		349. .672	
FT		/cag= g	
FT	primer_bind	/label= VK NO10/12.5	
FT		complement(438. .456)	
FT		/cag= i	
FT	primer_bind	/label= NO10KPRB	
FT		complement(628. .648)	
FT		/cag= j	
FT	primer_bind	/label= WOkappasFORNES	
FT		complement(650. .672)	
FT		/cag= k	
FT		/label= MOJkappasFOR2	
XX			
PN	W09303151-A1.		
XX			
XX	18-FEB-1993.		
XX			
PF	10-AUG-1992;	92WO-GB001483.	
XX			
PR	10-AUG-1991;	91GB-00017352.	
PR	11-JUN-1992;	92GB-00012419.	
XX			
PA	(MED1-) MEDICAL RES COUNCIL.		
PI	Embleton MJ, Gorochov G, Jones PT, Winter GP;		
DR	WPI; 1993-076508/09.		
XX	P-PSDB; AAR32841.		
PT	Treatment of cell populations, partic. hybridomas - to link together		
XX	copies of 2 or more non-contiguous DNA sequences to facilitate analysis.		
XX			
PS	Disclosure; Fig 3; 72pp; English.		
XX			
CC	The sequences given in AAQ37459-62 show the nucleotide sequences of		
CC	mature heavy chain VH domains and the VK light chain genes of the		
CC	antihenyloxazone hyridomas NO2/12.4 and NO10/12.5 which have been		
CC	linked via a linker peptide by in-cell PCR. The cDNA was synthesized		
CC	using forward primers annealing to the CK gene and the JH segment,		
CC	followed by assembly with linker primers, VH back primers based on the		
CC	VH1 leader sequence and a forward CK primer nested in respect to the		
CC	primer used for cDNA. The assembled product within the cells is then		
CC	amplified with nested primers annealing to the 5' end of the VH gene and		
CC	the 3' end of the JK segment. In-cell PCR may be used to determine gene		
CC	linkage analysis, particularly for the cloning of gene combinations that		
CC	are polymorphic within a population of cells, such as the rearranged		
CC	genes for Ig or TCR V regions. (Updated on 25-MAR-2003 to correct PN		
CC	field.)		
XX			
SQ	Sequence 672 BP; 161 A; 169 C; 184 G; 158 T; 0 U; 0 Other;		
Query Match	61.1%; Score 580.6; DB 2; Length 672;		
Best Local Similarity	91.1%; Pred. No. 3.6e-144;		
Matches 644; Conservative 0; Mismatches 24; Indels 39; Gaps 1;			
7 GAGGTCAAGCTGCAGAGTACGGGGAAGGCTTAGTGAGCCTGGAGGATCCCGAAATTC 66			
1 GATTGTGACGTGTCGAGACTTCGGGGGAGAGCTTTAATGACAGCTTGAGAGGATCCCAGAAATTC 60			



```

QY 445 CCAGCATCATGCTGTCATCTCCAGGGGAGAGGATCACCATGACTGACGTGCGCACTTCA 474
DB 481 CCATCTCTATGCTGCTGATCTGTAGGGGATCCGGGTCAACATGACCTGCGAGTGCAGCTCA 540
QY 475 AGCTTAGAGTAC-----TGAACGTGGTTCACAGAGTCAAGCACTCCGCCAAGA 528
DB 541 AGAATAGTATCCAGCAATTTGCACTGGTACCAAGAGTCAAGAACTTCCCCCAACC 600
QY 529 TGGATTATGACATCCAAAGCTGTCTGAGTCCCTGCTGCTTCACTGAGTCACTGG 588
DB 601 TGAATTATGACATCCAACTGCTGCTGAGTCCCTTCTGCTGAGTCACTGCACTGA 660
QY 589 TCTGGACCTCTTACTCTCTCACAATCAGACGATGAGGCTGAAGTCTGCGCACTTAC 648
DB 661 TCTGGACCGATTATACCTCAATCAGACGATGAGGCTGAAGTCTGCGCACTTAT 720
QY 649 TACTGCCAGAGTGAAGTAACTCACTGCTGCTGCTGGAACCAAGCTGAGCTG 708
DB 721 TACTGTCAACAGTGAAGTATTCACATCACTGCTGCTGAGGAGCAAGCTGAGCTG 780
QY 709 AAACGGGC 716
DB 781 AAACGGAC 788

RESULT 14
AA01652
ID AA01652 standard; DNA; 1668 BP.
XX AA01652;
AC 10-MAY-1999 (first entry)
XX 10-MAY-1999 (first entry)
DT 10-MAY-1999 (first entry)
XX Bispecific tetravalent antibody B17Ab10-B7-24H6 DNA.
DE Bispecific tetravalent antibody B17Ab10-B7-24H6 DNA.
XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
XX T cell activation; inhibitor; graft versus host disease;
XX transplant rejection; allograft rejection; autoimmune disease; allergy;
XX therapy; human; bispecific tetravalent antibody; B17Ab;
XX B17Ab10-B7-24H6; ss.
XX Mus BP.
XX Homo sapiens.
XX Synthetic.
XX Chimeric.
XX WO9858965-A2.
XX 30-DEC-1998.
XX 22-JUN-1998; 98WO-EP003791.
XX 20-JUN-1997; 97EP-00870092.
XX (INNO-) INNOGENETICS NV.
XX Lorie K, Sablon E, Buysse M, Bosman A;
XX WPI; 1999-105615/09.
XX P-PSDB; AAW90218.
XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat
XX immune diseases including allograft rejection.
XX Example 7.1; Fig 17; 182pp; English.
XX This DNA sequence encodes the bispecific tetravalent antibody B17Ab10-B7
XX -24H6 (see AAW90218) comprising the anti-B7.2 murine monoclonal antibody
XX (MAB) 1G10 VH region joined, via a flexible synthetic linker, to the 1G10
XX VL region, the human IgG3 hinge region, a helix-turn-helix dimerisation
XX domain, the human IgG3 hinge domain, the anti-B7.1 MAB B7-24 VH region,
XX another flexible linker, the B7-24 VL region and a hexahistidine tag. The

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CC B17Ab has been expressed in Escherichia coli cells. It cross-links,
CC and/or cross-reacts, with the costimulatory molecules B7.1 and B7.2
CC expressed on the membrane of professional antigen-presenting cells,
CC leading to the inhibition of antigen-specific T cell activation. The
CC invention relates to such B7-binding molecules, methods for their
CC production, and their use for treating or preventing diseases of the
CC immune system, in particular graft rejection, graft versus host disease,
CC allergy and autoimmune diseases (claimed)
XX
SQ Sequence 1668 BP; 409 A; 424 C; 453 G; 382 T; 0 U; 0 Other;
Query Match 56.7%; Score 539; DB 2; Length 1668;
Best Local Similarity 86.5%; Pred. No. 5.9e-133;
Matches 622; Conservative 0; Mismatches 85; Indels 12; Gaps 2;
QY 8 AGGTCAAGTGCAGAGTCAAGGGGAGGCTTGTGAGCTGAGAGGCTCCGGAACCTCT 67
DB 932 AGGTGACGCTACAGAGTCTGGGGAGGCTTGTGAGCTGAGAGGCTCCGCGCTCT 991
QY 68 CCTGTCAAGCTCTGATTCATCTTCAAGTCTTGAATGCACTGGTTCGTCAGGCTC 127
DB 992 CCGTGCACCTCTGATTCATCTTCAAGTCTTGAATGCACTGGTTCGTCAGGCTC 1051
QY 128 CAGAGAGGGGCTGAGTGGGCTGCATATATATATATATATATATATATATATAT 187
DB 1052 CAGGAGAGGGGCTGAGTGGGCTGCATATATATATATATATATATATATATAT 1111
QY 188 CAGACACATGAAAGGAGACATTCACATCTCCAGAGACAAATCCAGAACACCTCTTC 247
DB 1112 CAGACTCAGTGAAGGGGCGATTCACATCTCCAGAGACAAATGCAACACCTCTTC 1171
QY 248 TGCATATGACACAGTCTAAGTCTGAGACACGGTCAATATATATATATATATATAT 302
DB 1172 TGCATATGACACAGTCTAAGTCTGAGACACGGTCAATATATATATATATATAT 1231
QY 303 -TTACGGGCTTATTTGGGCGCAAGGAGCAACGGTCAACGGTCTCTCAAGTGAAGGCGCT 361
DB 1232 GGTACTTCATGCTGAGGCGCAAGGAGCAACGGTCAACGGTCTCTCAAGTGAAGGCGCT 1291
QY 362 CAGGCGGAGTGGCTCTGCGGCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 421
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QY 422 TCATGCTGATCTCCAGGGGAGAGGGTCAACATCTGACGTGACGTCAAGTGA 481
DB 1352 CTRAGCTGATCTGAGGGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 1411
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QY 536 ATGACATCTCAAACTGTCTTCTGAGTCCCTGCTGCTTCAATGAGTGGTCTGGGA 595
DB 1472 ATGACATCTCAAACTGTCTTCTGAGTCCCTGCTGCTTCAATGAGTGGTCTGGGA 1531
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DB 1532 CGATTATACCTTCAACATCAGACGATGAGGCTGAAGTGTGCACTTACTATGCC 1591
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DB 1592 AACAGTGAAGTAACTCACTGAGTGGTCTGAGACCAAGCTGAGATCAACCG 1650

RESULT 15
AADS8607
ID AADS8607 standard; DNA; 711 BP.
XX AADS8607;
AC AADS8607;
XX 04-DEC-2003 (first entry)
XX Mouse G1 single chain Fv-recombinant antibody DNA.

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XX Major histocompatibility complex; MHC; HLA-restricted antigen; cancer;  
KW viral infection; autoimmune disease; gene therapy; cytostatic; virucide;  
KW immunomodulator; mouse; gene; ds.  
OS Mus sp.  
FH Key Location/Qualifiers  
FT CDS 1..711  
FT /tag= a  
FT /product= "Mouse GI single chain Fv-recombinant antibody"  
FT /note= "No start and stop codon"  
FT /partial  
XX WO2003068201-A2.  
XX 21-AUG-2003.  
XX PD 11-FEB-2003; 2003WO-IL000105.  
XX PR 13-FEB-2002; 2002US-00073301.  
XX PA (TECR ) TECHNION RES & DEV FOUND LTD.  
XX PI Reiter Y, Denberg G;  
XX WI; 2003-689603/65.  
XX DR P-PSDB; AAE38657.  
XX PT New isolated molecule comprising an antibody that binds with a human  
PT major histocompatibility complex (MHC) class I being complexed with a HLA  
PT -restricted antigen, useful for treating cancer, viral infection or  
PT autoimmune disease.  
XX PS Claim 62; Fig 3a; 81pp; English.  
XX CC The invention relates to an isolated molecule comprising an antibody  
CC specifically bindable with a binding affinity below 20 nanomolar to a  
CC human major histocompatibility complex (MHC) class I being complexed with  
CC a HLA-restricted antigen. The molecules, antibodies, and methods are  
CC useful for treating cancer, viral infection and an autoimmune disease.  
CC The invention is useful in gene therapy. The present sequence is mouse GI  
CC single chain Fv-recombinant antibody DNA  
XX SQ Sequence 711 BP; 164 A; 176 C; 208 G; 163 T; 0 U; 0 Other;  
Query Match 56.0%; Score 532.4; DB 9; Length 711;  
Best Local Similarity 85.8%; Pred. No. 2.5e-131;  
Matches 609; Conservative 0; Mismatches 86; Indels 15; Gaps 1;  
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QY 353 GAGGCGCTCAGAGCGAGAGTGGCTCTGGCGGTGGCGGATTCGACATTTAGCTCACCCACT 412  
DB 362 GAGGCGTTCAGAGCGAGAGTGGCTCTGGCGGTGGCGGATTCGACATTTAGCTCACCTCAGT 421  
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QY 593 GGAACCTTTACTCTCTCAATTCAGACACATGAGAGCTGAAGATGCTCCACTTACTACT 652  
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QY 653 GCCAGCAGTGAAGTGAACCACTCAAGTTCGGTCTGGAGCAAGCTG 702  
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Job time : 621 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 09:03:52 ; Search time 689 Seconds  
(without alignments)  
8627.347 Million cell updates/sec

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Perfect score: 951  
Sequence: 1 atggccgaggtcagctgca.....ggcagaagaagcagctag 951

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Searched: 6067389 seqs, 3125258755 residues  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949	99.8	8902	17	US-10-221-276-5
2	460.2	48.4	807	16	US-10-408-930-4
3	459.6	48.3	873	18	US-10-406-830-36
4	448.8	47.2	726	15	US-10-259-087A-19
5	448.8	47.2	726	19	US-10-689-006-19
6	446	46.9	861	18	US-10-406-830-31
7	443.6	46.6	1176	15	US-10-075-947A-3

8	442	46.5	717	9	US-09-808-037-5	Sequence 5, Appl1
9	442	46.5	717	14	US-10-162-889-5	Sequence 5, Appl1
10	442	46.5	717	17	US-10-384-788-5	Sequence 5, Appl1
11	442	46.5	717	18	US-10-618-856-5	Sequence 5, Appl1
12	442	46.5	717	21	US-10-749-522-5	Sequence 5, Appl1
13	438.2	46.1	720	9	US-09-976-787-30	Sequence 30, Appl1
14	436	45.8	780	4	US-10-247-448-3	Sequence 3, Appl1
15	434.8	45.7	717	14	US-08-940-544-3	Sequence 3, Appl1
16	434.8	45.7	717	15	US-10-075-947A-1	Sequence 1, Appl1
17	434.2	45.7	717	21	US-10-688-255-6	Sequence 6, Appl1
18	434	45.6	873	18	US-10-406-830-35	Sequence 35, Appl1
19	433.8	45.6	714	10	US-09-798-689-22	Sequence 22, Appl1
20	430.6	45.3	714	9	US-09-976-787-31	Sequence 31, Appl1
21	430.6	45.3	711	14	US-10-247-448-1	Sequence 1, Appl1
22	428.6	45.1	786	19	US-10-689-006-23	Sequence 23, Appl1
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24	426.8	44.9	1673	10	US-09-819-266-27	Sequence 27, Appl1
25	424.2	44.6	723	18	US-10-062-188-4	Sequence 4, Appl1
26	422	44.4	732	21	US-10-879-994-15	Sequence 15, Appl1
27	422	44.4	732	21	US-10-610-452-15	Sequence 15, Appl1
28	421.6	44.3	726	15	US-10-259-087A-17	Sequence 17, Appl1
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31	417.4	43.9	768	18	US-10-239-656-60	Sequence 60, Appl1
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35	410	43.0	738	21	US-10-861-617-16	Sequence 16, Appl1
36	409.2	43.0	717	21	US-10-935-290-145	Sequence 145, Appl1
37	407	42.8	756	16	US-10-169-351-68	Sequence 68, Appl1
38	406.6	42.8	924	9	US-09-742-693-26	Sequence 26, Appl1
39	405.6	42.6	728	20	US-10-798-380-30	Sequence 30, Appl1
40	404.8	42.6	1479	19	US-10-682-845-66	Sequence 66, Appl1
41	404.8	42.6	1479	19	US-10-682-845-76	Sequence 76, Appl1
42	403.2	42.4	1241	18	US-10-362-591-1	Sequence 1, Appl1
43	403.2	42.4	1479	19	US-10-682-845-60	Sequence 60, Appl1
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## ALIGNMENTS

RESULT 1  
US-10-221-276-5  
; Sequence 5, Application US/10221276  
; Publication No. US20030211495A1  
; GENERAL INFORMATION:  
; APPLICANT: TWM Telethon Institute for Child Health Research  
; TITLE OF INVENTION: Improved Reverse Two Hybrid Screening Method  
; FILE REFERENCE: multiple reporter pct.doc  
; CURRENT APPLICATION NUMBER: US/10/221,276  
; CURRENT FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 8902  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1).....(8902)  
; OTHER INFORMATION: n = A, T, C or G  
; US-10-221-276-5

Query Match 99.8%; Score 949; DB 17; Length 8902;  
Best Local Similarity 99.8%; Pred. No. 1.7e-281;  
Matches 949; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
1 ATGCCGAGGTCAAGCTGACGAGTCAAGGAGGCTTACTGACGCTGAGGCTCCCG 60  
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QY 121 CAGGCTCCAGAGAGGAGGCTGAGTGGTTCGATATATTAATGAGTGGAGTACATC 180  
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Db 3720 ATCATCTCTCTATCATCTCTCATCATGCTTTGGCAGAGAGCAAGCTTAA 3770

RESULT 2  
US-10-408-930-4  
; Sequence 4, Application US/10408930  
; Publication No. US20030170820A1  
; GENERAL INFORMATION:  
; APPLICANT: Coia, et al.  
; TITLE OF INVENTION: CONTINUOUS IN-VITRO EVOLUTION  
; FILE REFERENCE: 674537-2003.1  
; CURRENT APPLICATION NUMBER: US/10/408, 930  
; CURRENT FILING DATE: 2003-04-07

PRIOR APPLICATION NUMBER: PCT/AU99/00341  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 09/674,677  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: AU P23445  
; PRIOR FILING DATE: 1998-05-08  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 807  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(807)  
; OTHER INFORMATION: Sequence of the anti-hepatitis surface antigen (4c2) scFv  
US-10-408-930-4

Query Match 48.4%; Score 460.2; DB 16; Length 807;  
Best Local Similarity 77.5%; Pred. No. 4e-131;  
Matches 574; Conservative 0; Mismatches 156; Indels 9; Gaps 1;

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? Sequence 19, Application US/10689006
? Publication No. US20040191249A1
? GENERAL INFORMATION:
? APPLICANT: Vanderbilt University
? APPLICANT: Hallahan, Dennis E
? APPLICANT: Mernaugh, Raymond
? TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
? FILE REFERENCE: 1242/72
? CURRENT APPLICATION NUMBER: US/10/689,006
? CURRENT FILING DATE: 2003-10-20
? PRIOR APPLICATION NUMBER: US 09/914,605
? PRIOR FILING DATE: 2001-08-30
? PRIOR APPLICATION NUMBER: US 10/259,087
? PRIOR FILING DATE: 2002-09-27
? NUMBER OF SEQ ID NOS: 34
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 19
? LENGTH: 726
? TYPE: DNA
? ORGANISM: Artificial
? FEATURE:
? OTHER INFORMATION: Artificial antibody ligand number 2
? NAME/KEY: CDS
? LOCATION: (1)..(726)
? US-10-689-006-19

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Best Local Similarly	77.4%	Pred. NO. 1.3e-127		
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QY 61 AAACCTCCTCGTGCAGCCTCTGGATTCACTTTCAGTACCTTGGAGATGCATGGGTCGT 120

Db 61 AAATGTCCTCGCAGAGCTTCTGSAATACAACTTCACTACCTAATGTTATGCACTGGGTGAAG 120

QY 121 CAGGCTCCAGAGAAAGGGGCTGGAGTGGGGTCGCAATATTAGAGTGGCAGTAGACATC 180

Db 121 CAGAGCCTTGGCAGGGGCTTGAAGTGGATTGATTAATTCCTTCAATATGATGTACT 180

QY	181	TCTATGACGACACAGTGAAGGGAGATTCACATCTCCAGAGACATCTCCAAAGACCC	240
Db	181	AAGTACATAGAAAGTTCAAAGGCAAGGCCGCACTGACTTCAGACAAATCTCCAGACA	240
QY	241	CTGTTCCTTGCAAAATGACCAAGTCTTAAGGCTTGAGGACACGGTCATGATTTACTGTGCAAGA	300
Db	241	GCTCATATGAGACTCAGACGCTGACCTCTGAGGACTCTGGGGCTATTAATCTGTGCAAGA	300
QY	301	-----GATTACGGGGCTTATTGGGGCCAAAGGACCAAGGTCAACGGTCAACGGTCTCTCA	348
Db	301	TTTGGTAACTACGGGTCTTTGGACTAGTGGGCGCAAGGGACCAAGGTCAACGGTCTCTCA	360
QY	349	GGTGAAGGCGGCTCAGCGGAGATGAGCTTGGCGGTGAGCGGATTCGACATTGAGCTCAC	408
Db	361	GGTGAAGGCGGTTCAAGGCGGAGGTGGCTTGGCGGTGAGCGGATTCGACATTGAGCTCAC	420
QY	409	CAGTCTCCAGCAATCATGTTCGACTTTCAGAGGGAGAGGGTCACATGACTGCAAGTGC	468
Db	421	CAGTCTCCAAACATCATGTCTGCATCTCCAGGGAGAAAGGTCAACATTAACCTGAGTGC	480
QY	469	AGTTCAGAGTAAAGTACATGAATCTGGTTCCAACAGAAATCAGGCACTCTCCCAAAAGA	528
Db	481	AGTTCAGAGTAAAGTACATGACATCGGTTCCAGAGAAAGCAGGCACTTCTCCAAACC	540
QY	529	TGGATTATGACACATCCAAACTGTCTTGGAGTCCCTGCTCAGTGGCAAGTGG	588
Db	541	TGGATTATGACACATCCAACTGGCTTCTGGAGTCCCTGTTCGCTTCAATGGGCAATGGA	600
QY	589	TCTGGAGCTCTTACTCTCTCACAATCAGCAGCATGAGGCTGAAAGTGTGCACTTAC	648
Db	601	TCTGGAGCTCTTATTCTCTCACAATCAGCAGCATGAGGCTGAAAGTGTGCACTTAT	660
QY	649	TACTCCAGCAGTGAAGTAAAGTAAACCACTCAGTTCCGTGCTGGGACCAAGCTGGAAGCTG	708
Db	661	TACTGTCAACAGTGAAGTAAATTAACCACTCAGTTCCGAGGGGACCAAGCTGGAATA	720
QY	709	AAACGG 714	
Db	721	AAACGG 726	

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RESULT 6
US-10-406-830-31
; Sequence 31, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-10-406-830-31

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Query Match 46.9%; Score 446; DB 18; Length 861;  
Best Local Similarity 74.6%; Pred. No. 9.9e-127;  
Matches 595; Conservative 185; Indels 18; Gaps 2.

QY 1 ATGCCCAAGCTCAAGCTCAGAGACTCAGGGGAGGCTTAAAGCAGCCTCGAGGGTCCCCG 60  
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120      61  ATGGCCAGGTGCAGCTGGTGGAGTCTGGGAGGAGGGGTGGTCCAGCTGGGAAGTCCCTG 120
121      61  AAATCTCTCTGTGACAGCTCTGTGGATCACTTTCAAGTAGCTTTGGAATGCACTGGGTTGGT 120
122      Db  121  AGACTCTCTGTGACAGCTCTGTGGATCACTTTCAAGTAGCTTTGGAATGCACTGGGTTGGT 180
123      Qy  121  CAGGCTCCAGAAAGGGGGCTGGAGTGGGTGGCAATAATTAGTAGTGGAGTAGTACCATC 180
124      Db  181  CAGGCTCCAGAAAGGGGGCTGGAGTGGGTGGCAAGTATTATTCATATATAGCAATTAATAA 240
125      Qy  181  TACTATGACAGACAGTGAAGGGAACGATTCACCATCTCCAGAGACATCCCAAGAACCC 240
126      Db  241  TACTAGCGCGCTCCGTGTAAGAACCATTCACCATCTCCAGAGACATTCAGAAACAG 300
127      Qy  241  CTGTTCTCTGCAAAATGACCAAGTCTTAAGTCTTGAGAGACAGCGTCATGATTACTGTGAGA 300
128      Db  301  GTGTCTCTGCAAAATGAAACAGCTTGAGAGCTTGAGAGACACGGCTGTGATTACTGTGAGA 360
129      Qy  301  GATTACGGGGCT-----TATTGGGGGCCAAGGGAACCAAGGTCAACCGTCTCC 345
130      Db  361  GATCTCTACGGGTGACTACGCTCTTTGACTATCTGGGGGCAAGGAAACCTGTGACCGTCTCC 420
131      Qy  346  TCAGGTGAGAGCGGCTCAGAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGCATTTGAGCTC 405
132      Db  421  TCAGGTGAGAGCGGCTCAGAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGCATTCAGATG 480
133      Qy  406  ACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGAGAGGGTCAACATGACCTGCAAT 465
134      Db  481  ACCCAGTCTCTTCCACCCCTGTCTGGCATCTCTGGGAGACAGAGTCAACATCATTTGCCGG 540
135      Qy  466  GCCAGTTCAAG---TGTAAGGTATCATGAATCTGTTCCACAGAAAGTCAGCACTTCCCC 522
136      Db  541  GCCAGTCAGAGTATGTGTGATGCTGTGGTGGCTGGTATCACACAGAAACAGGAAAGCCCT 600
137      Qy  523  AAAAGATGAGATTATGACACATCCAAACTGTCTTCTGAGTCCCTGCTCGCTTCAGTGGC 582
138      Db  601  AAATCTCTGATCTATATAGCGCTCTACTTTAGAAAGTGGGGTCCCATCAAGGTTCAACGGC 660
139      Qy  583  AGTGGGTCTGGGACCTCTTACTCTCTCACAATTCAGCAGATGGAGGCTGAAGTGTGCC 642
140      Db  661  AGTGATCTGGGACAGAAATTACTCTCACAATTCAGCGGCTCCAGCTGAAGATTTTGGCA 720
141      Qy  643  ACTTACTACTGCGCAGACGTGGAGTAGTAACCCACTCACTGTTGGTCTGGGACCAAGCTG 702
142      Db  721  ACTTATTCTGTCAAGAGCTTATGATTACCCGCTCACTTTCGGCGGAGGACCAAGGTG 780
143      Qy  703  GAGCTGAAGCGGGCGGCGCAGAAACAAAACATCATCTCAGAAAGAGATCGAATGGGGCC 762
144      Db  781  GAATCAAAACGTGGCGCGCAGAAACAAAACATCATCTCAGAAAGAGATCGAATGGGGCC 840
145      Qy  763  GTCCAGCAACAAAATCTC 780
146      Db  841  GCACATCACATCATCAC 858
147
148      RESULT 7
149      US-10-075-947A-3
150      : Sequence 3, Application US//10075947A
151      : Publication No. US20030147808A1
152      : GENERAL INFORMATION:
153      : APPLICANT: Cheung, Nai-Kong V.
154      : APPLICANT: Larson, Steven M.
155      : APPLICANT: Guo, Hong-Fen
156      : APPLICANT: Rivlin, Ken
157      : APPLICANT: Sadelain, Michel
158      : TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
159      : FILE OF INVENTION: Antibodies
160      : FILE REFERENCE: MSK.P-013-2
161      : CURRENT APPLICATION NUMBER: US/10/075, 947A
162      : CURRENT FILING DATE: 2002-02-13
163      : PRIOR APPLICATION NUMBER: 09/142, 974
164      : PRIOR FILING DATE: 1998-09-18
165      : PRIOR APPLICATION NUMBER: PCT/US97/04427

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1  PRIOR FILING DATE: 1997-03-20
2  PRIOR APPLICATION NUMBER: 60/013,703
3  PRIOR FILING DATE: 1996-03-20
4  NUMBER OF SEQ ID NOS: 5
5  SOFTWARE: PatentIn Ver. 2.1
6  SEQ ID NO: 3
7  LENGTH: 1176
8  TYPE: DNA
9  ORGANISM: Murine
10 OTHER INFORMATION: 5fl-scFv-streptavidin
11 FEATURE:
12 NAME/KEY: unsure
13 LOCATION: (37)
14 FEATURE:
15 NAME/KEY: unsure
16 LOCATION: (73)
17 OS: 10-075-947A-3

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Query Match	46.6%;	Score 443.6;	DB 15;	Length 1176;
Best Local Similarity	76.6%;	Pred. No. 6e-126;		
Matches 558; Conservative	0;	Mismatches 161;	Indels 9;	Gaps 1;

Qy	8	AGGTCAAGCTGCAGAGGATCAGGGGAGGCTTAGTGTACACCTGGAGGGGTCCGGAACCTCT	67
Db	2	AGGTGAAATCTGCAGCAGTCAGGAACTGAACTGTGTAGACCTCTGGGCTTCACTGAAGATAT	61
Qy	68	CTGTGTACACCTCTGGATTCACTTTCACTAGCTTGGATGCACTGGGTGTGTGAGGCTC	127
Db	62	CTGCAAGACTTCTGGANCAAAATTCATCAATGAATACCATGATGCACTGGGGTGAAGAGAGCC	123
Qy	128	CAGAGAAAGGGCTCGAGTGGGTTCGCATATATTAGTAGTGGCAGTAGTACCATCTATATG	187
Db	122	ATGGAAGAAGCCTTAGTGTGATTTGAGGATTTAACTTCAACAATGGTGTACTAATTCA	183
Qy	188	CAGACACAGTGAAGGGACGATTCACCATCTCCAGAGCAATCCCAAGAACCCCTGTCTC	247
Db	182	AGCAGAAAGTTCAAGGGCAAGGGCCATTTAGCTGTAGACAAAGTCTCCAGACAGACCTACA	243
Qy	248	TGCAAAATGACACAGTCTAAGGTCTGAGACACGGTCACTATTTACTGTGCAGAGATTACG	307
Db	242	TGGAGTCCGCGACGCTGACATCTGAGGATTCGTGCAGTCTAATTACTGTCCAAAGACTACTA	303
Qy	308	GG-----GCTATTGGGGGCAAGGGACCAAGGTCACGGTCAACGCTCTCAAGTGAAGCG	358
Db	302	CGGTCCCGTTTGCTTACTGGGTCCAAAGGACCAAGGTCAACGGTCTCTCAAGTGAAGCG	364
Qy	359	GCTCAGCGGAGGTGGCTCTGCGGGTGGCGGATCGGACATTGAAGTCAACCAAGTCTCCAG	418
Db	362	GTTCAAGCGGAGGTGGCTCTGCGGGTGGCGGATCGGACATGAGGTCACTCAAGTCTCCAG	424
Qy	419	CAATCATGTCTGCATTTCCAGGGGAGAGGGTCACATGACTCGCAGTGGCCAGTTCAAGTG	477
Db	422	CAATCATGTCTGCATTTCCAGGGGAGAGAGTCAACATGACCTGAGTGGACGTCACAGTA	483
Qy	479	TAAGTATACATGAATCTGGTCCAAACGAAGTACGAGCACTCCGCCAAAGATGATTTATG	538
Db	482	TAAGTATACATGACATGTGTACAGAGAAAGCCTGTCACTCCGCCAAAGATGATTTATG	544
Qy	539	ACAACATCCAACTGTCTTCTGGAGTCCCTGTCTGCTTCAGTGGCAGTGGGTCTGTGGACCT	598
Db	542	ACAACATCCAACTGTGCTTCTGGAGTCCCTGTCTGCTTCAGTGGCAGTGGGTCTGTGGACCT	604
Qy	599	CTTACTCTCTCAATCAGACAGACATGAGAGGCTGAAAGTGGCCACTTACATCTGCGACG	658
Db	602	CTTATTCTCTCAACATCAGACAGACATGAGAGGCTGATGATGTGCGCACTTATTACTGCCATC	664
Qy	659	AGTGAAGTAGTAACCACTCAACGTTCTGGTCTGGAGCCAACTGGAGCTGTAAACGGGCGG	718
Db	662	AGCGAGTAGTATTACCGGCTCAAGTTCTGGTCTGGAGCCAACTGGAGTGTAAACGGGCGG	724
Qy	719	CCGCGAAG 726	

Db 722 CCGCTGA 729

RESULT 8  
US-09-808-037-5  
; Sequence 5, Application US/09808037  
; Patent No. US2002005211A1  
; GENERAL INFORMATION:  
; APPLICANT: SOLOMON, Beke  
; APPLICANT: HANAN, Eliat  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF  
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS  
; FILE REFERENCE: SOLOMON-2D  
; CURRENT APPLICATION NUMBER: US/09/808,037  
; CURRENT FILING DATE: 2001-03-15  
; PRIOR APPLICATION NUMBER: 09/629,971  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 09/473,653  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: US 60/152,417  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 717  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(717)  
US-09-808-037-5

Query Match 46.5%; Score 442; DB 9; Length 717;  
Best Local Similarity 77.4%; Pred. No. 1,6e-125;  
Matches 554; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 8 AGGTCAAGTGAAGAGTGAAGAGGAGGCTTAGTGAAGCTTGAAGGCTCCGGAACCT 67  
DB 2 AGGTCAAACTGAGAGAGTGAAGGAGGCTGAGCTGAGGCTGAGGCTTGAAGGATTT 61  
QY 68 CCGTGAAGCTCTGAGATTCATCTTCAAGTCTTGAAGTGAAGTGAAGTCTGAGGCTC 127  
DB 62 CCGTGAAGGCTCTGAGATTCATCTTCAAGTCTTGAAGTGAAGTGAAGTCTGAGGCTC 121  
QY 128 CAGAGAGGAGGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 187  
DB 122 ATGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 181  
QY 188 CAGACAGAGTGAAGAGGAGATTCATCTTCAAGAGCAATCCCAAGAACACCCGTTCC 247  
DB 182 ACCAGAAATTGAAGGAGCAAGGAGCAATGATCTGAGCAAAATCTCCAGACAGAGCTATA 241  
QY 248 TSCAATGACAGCTTAAGTCTGAGAGCAAGGATCATGATTAATGATGAGAGG----- 301  
DB 242 TGAAGTCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 301  
QY 302 -----ATTACGGGGCTTAATGAGGAGCAAGGAGCAAGGAGCAAGGAGCAAGGAGGAG 355  
DB 302 CTATGCTCTACTTTGATCTGAGGAGCAAGTGAAGCAAGGAGCAAGGAGGAGGAG 361  
QY 356 GGGGCTCAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 415  
DB 362 GGGGCTCAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 421  
QY 416 CAGCAATCATGCTGATCTCAGAGGAGAGAGGATCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 475  
DB 422 CAGCAATCATGCTGATCTCAGAGGAGAGAGGATCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 481  
QY 476 GTGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 535  
DB 482 GTATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 541  
QY 536 ATGACATCATCAAACTGCTTCTGAGAGTCCGCTGCTTCAAGTGAAGTGAAGTGAAGTGAAG 595

Db 542 ATGACATCATCAAACTGCTTCTGAGAGTCCCTGCTGCTTCAAGTGAAGTGAAGTGAAGTGAAG 601  
QY 536 CCGTCTACTCTCAATCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 655  
DB 602 CCGTCTACTCTCAATCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 661  
QY 656 AGCAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 711  
DB 662 ATGACGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 717

RESULT 9  
US-10-162-889-5  
; Sequence 5, Application US/10162889  
; Publication No. US20030077252A1  
; GENERAL INFORMATION:  
; APPLICANT: SOLOMON, Beke  
; APPLICANT: HANAN, Eliat  
; TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME  
; TITLE OF INVENTION: USEFUL IN DIAGNOSING  
; TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES  
; FILE REFERENCE: SOLOMON-2B  
; CURRENT APPLICATION NUMBER: US/10/162,889  
; CURRENT FILING DATE: 2002-06-06  
; PRIOR APPLICATION NUMBER: US/09/629,971  
; PRIOR FILING DATE: 2000-07-31  
; PRIOR APPLICATION NUMBER: US 09/473,653  
; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: US 60/152,417  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 717  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(717)  
US-10-162-889-5

Query Match 46.5%; Score 442; DB 14; Length 717;  
Best Local Similarity 77.4%; Pred. No. 1,6e-125;  
Matches 554; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 8 AGGTCAAGTGAAGAGTGAAGAGGAGGCTTAGTGAAGCTTGAAGGCTCCGGAACCT 67  
DB 2 AGGTCAAACTGAGAGAGTGAAGGAGGCTGAGCTGAGGCTGAGGCTTGAAGGATTT 61  
QY 68 CCGTGAAGCTCTGAGATTCATCTTCAAGTCTTGAAGTGAAGTGAAGTGAAGTCTGAGGCTC 127  
DB 62 CCGTGAAGGCTCTGAGATTCATCTTCAAGTCTTGAAGTGAAGTGAAGTGAAGTCTGAGGCTC 121  
QY 128 CAGAGAGGAGGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 187  
DB 122 ATGCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 181  
QY 188 CAGACAGTGAAGAGGAGATTCATCTTCAAGAGCAATCCCAAGAACACCCGTTCC 247  
DB 182 ACCAGAAATTGAAGGAGCAAGGAGCAATGATCTGAGCAAAATCTCCAGACAGAGCTATA 241  
QY 248 TSCAATGACAGCTTAAGTCTGAGAGCAAGGATCATGATTAATGATGAGAGG----- 301  
DB 242 TGAAGTCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 301  
QY 302 -----ATTACGGGGCTTAATGAGGAGCAAGGAGCAAGGAGCAAGGAGCAAGGAGGAG 355  
DB 302 CTATGCTCTACTTTGATCTGAGGAGCAAGTGAAGCAAGGAGCAAGGAGGAGGAG 361  
QY 362 GGGGCTCAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 415  
DB 362 GGGGCTCAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 421

QY 416 CAGCAATCATGTCATCTCCAGGGAGAGGCTCAACATGACCTTCAGTCCAGTTCAA 475  
 DB 422 CAGCAATCATGTCATCTCCAGGGAGAGGCTCAACATGACCTTCAGTCCAGTTCAA 481  
 QY 476 GTGTAAAGTACATGAACTGTTCCACAGAAAGTCAAGGACCTCCCAAAAGATGATTT 535  
 DB 482 GTATAAGTACATGAACTGTTCCACAGAAAGTCAAGGACCTCCCAAAAGATGATTT 541  
 QY 536 ATGACATCATCAAACTGTCTTCTGAGTCCCTGCTGCTTCAAGTGGAGTGGGCTGGGA 595  
 DB 542 ATGACATCATCAAACTGTCTTCTGAGTCCCTGCTGCTTCAAGTGGAGTGGGCTGGGA 601  
 QY 596 CCTCTTACTCTCTCAACATCAGCAGCAGTGAAGCTGAAGTGTGCACTTACTACTGCC 655  
 DB 602 CCTCTTACTCTCTCAACATCAGCAGCAGTGAAGCTGAAGTGTGCACTTACTACTGCC 661  
 QY 656 AGCAGTGAAGTGAATCCCACTCAAGTGTGGTCTGGAGCAACAACTGAGCTGAAA 711  
 DB 662 ATCAGCGAGTGAATCCCACTCAAGTGTGGAGGAGGAGCAAGCTGAGAAATGAAA 717

RESULT 10

US-10-384-788-5  
 ; Sequence 5, Application US/10384788  
 ; Publication No. US20040013647A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOLOMON, Bekka  
 ; APPLICANT: FRENKEL, Dan  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE  
 ; FILE REFERENCE: SOLOMON=2D.2  
 ; CURRENT APPLICATION NUMBER: US/10/384,788  
 ; CURRENT FILING DATE: 2003-03-11  
 ; PRIOR APPLICATION NUMBER: 60/371,735  
 ; PRIOR FILING DATE: 2002-04-12  
 ; PRIOR APPLICATION NUMBER: 09/808,037  
 ; PRIOR FILING DATE: 2001-03-15  
 ; PRIOR APPLICATION NUMBER: 09/830,954  
 ; PRIOR FILING DATE: 2001-06-22  
 ; PRIOR APPLICATION NUMBER: 10/162,889  
 ; PRIOR FILING DATE: 2002-06-06  
 ; PRIOR APPLICATION NUMBER: 09/473,653  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: 09/629,971  
 ; PRIOR FILING DATE: 2000-07-31  
 ; PRIOR APPLICATION NUMBER: 60/152,417  
 ; PRIOR FILING DATE: 1999-09-03  
 ; PRIOR APPLICATION NUMBER: PCT/IL00/00518  
 ; PRIOR FILING DATE: 2000-08-31  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 5  
 ; LENGTH: 717  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(717)  
 ; US-10-384-788-5

Query Match 46.5%; Score 442; DB 17; Length 717;  
 Best Local Similarity 77.4%; Pred. No. 1,6e-125;  
 Matches 554; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 8 AGGTCAAGTGCAGAGTCAAGGGAGGCTTACTGACAGCTGAGGGCTCCCGAAACTCT 67  
 DB 2 AGGTCAAACTGCAGAGTCAAGGGAGGCTTACTGACAGCTGAGGGCTCCCGAAAGATTT 61  
 QY 68 CCTGTCAAGCTTGTGATTTCACTTTAGTACGCTTTGGAATGACCTGGGTTCTGAGGCTC 127  
 DB 62 CCTGTCAAGGTTCTGTCTTACATTTCACTGATTTATCTTAACTGAGCTGGGTTGAAACAGATTC 121  
 QY 128 CAGAGAAAGGGGCTGAGTGGGTGCAATATATATAGTGGCACTAGTACATCTACTATG 187

DB 122 ATGCAAGAGTCTAGAGTGAATTTAGTATTAAGTAACTTACTATGATGTGATGCTAGTACA 181  
 QY 188 CAGACACAGTGAAGGAGCATTTACCATCTCCAGAGACAAATCCCAAGAACCCCTGTCC 247  
 DB 182 ACCAAGAGTTCAAGGCAAGGCAACATATGATGTAGACAAATCTCCAGACAGCTTAA 241  
 QY 248 TGCAGAAATGACAGTCAAGTCTGAGACAGGTCATGATTAATCTGTGCAAGAG----- 301  
 DB 242 TGGAACTCCAGACTGACATCTGAGAGTTCTGCCATCTATTACTGTGCAAGAGGGGCTA 301  
 QY 302 -----ATTACGGGGCTTATTTGGGGCCAGAGGACACCGTCACTCTCTCAAGTGGAG 355  
 DB 302 CTATGTCTTACTTTGATCTGCTGGGGCCAAAGTACACAGGTCACCGTCTCTCAAGTGGAG 361  
 QY 356 GGGGCTCAGGCGGAGGCTGCTGGGGGGGGGAGATGGACATTTGAGCTCACCAAGTCTC 415  
 DB 362 GGGGCTCAGGCGGAGGCTGCTGGGGGGGGGAGATGGACATTTGAGCTCACCAAGTCTC 421  
 QY 416 CAGCAATCATGTCATCTCCAGGGAGAGGCTCAACATGACCTTCAGTCCAGTTCAA 475  
 DB 422 CAGCAATCATGTCATCTCCAGGGAGAGGCTCAACATGACCTTCAGTCCAGTTCAA 481  
 QY 476 GTGTAAAGTACATGAACTGTTCCACAGAAAGTCAAGGACCTCCCAAAAGATGATTT 535  
 DB 482 GTATAAGTACATGAACTGTTCCACAGAAAGTCAAGGACCTCCCAAAAGATGATTT 541  
 QY 536 ATGACATCATCAAACTGTCTTCTGAGTCCCTGCTGCTTCAAGTGGAGTGGGCTGGGA 595  
 DB 542 ATGACATCATCAAACTGTCTTCTGAGTCCCTGCTGCTTCAAGTGGAGTGGGCTGGGA 601  
 QY 596 CCTCTTACTCTCTCAACATCAGCAGCAGTGAAGCTGAAGTGTGCACTTACTACTGCC 655  
 DB 602 CCTCTTACTCTCTCAACATCAGCAGCAGTGAAGCTGAAGTGTGCACTTACTACTGCC 661  
 QY 656 AGCAGTGAAGTGAATCCCACTCAAGTGTGGTCTGGAGCAACAACTGAGCTGAAA 711  
 DB 662 ATCAGCGAGTGAATCCCACTCAAGTGTGGAGGAGGAGCAAGCTGAGAAATGAAA 717

RESULT 11

US-10-618-856-5  
 ; Sequence 5, Application US/10618856  
 ; Publication No. US20040052766A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SOLOMON, Bekka  
 ; APPLICANT: FRENKEL, Dan  
 ; TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY  
 ; FILE REFERENCE: SOLOMON=2A  
 ; CURRENT APPLICATION NUMBER: US/10/618,856  
 ; CURRENT FILING DATE: 2003-07-15  
 ; PRIOR APPLICATION NUMBER: 09/473,653A  
 ; PRIOR FILING DATE: 1999-12-29  
 ; PRIOR APPLICATION NUMBER: US 60/152,417  
 ; PRIOR FILING DATE: 1999-09-03  
 ; NUMBER OF SEQ ID NOS: 26  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 717  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(717)  
 ; US-10-618-856-5

Query Match 46.5%; Score 442; DB 18; Length 717;  
 Best Local Similarity 77.4%; Pred. No. 1,6e-125;  
 Matches 554; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

QY 8 AGGTCAAGTGCAGAGTCAAGGGAGGCTTACTGACAGCTGAGGGCTCCCGAAACTCT 67  
 DB 2 AGGTCAAACTGCAGAGTCAAGGGAGGCTTACTGACAGCTGAGGGCTCCCGAAAGATTT 61

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QY 68 CCTGTGACGCTCTGTGATTCACTTTGAGTAGCTTTGGAAATGCACTGGGTTCTGACGGCTC 127
|||
Db 62 CCTGCAAGGGTTCTGTGCTACACATTTACGATTTATGCTATGCACTGGGTAAGACAGAGTC 121
|||
QY 128 CAGAGAAAGGGGCTGAGGGTGTGCAATATATTAGTAGTGGAGTAGTACCATCTACTATG 187
|||
Db 122 ATGCAAAAGAGTGTAGAGTGTGATTTAGTTATTTAGTTACTATGATGTAGTACTATACA 181
|||
QY 188 CAGACACAGTGAAGGAGCAATTCACATCTCCAGAGACAATCCCAAGAACACCTGTTCC 247
|||
Db 182 ACCAGAAAGTTCAAGGCAAGGCCACATGACTGTAGACAAATCTCCACACAGCTTATA 241
|||
QY 248 TGCAAATGACAGTCTAAGTCTGAGAGACACCGTCTATTTATTTACTGTGCAAGAG----- 301
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Db 242 TGGAACTTGCACAGACTGACATCTGAGAGATTCTGCCATCTATTTACTGTGCAAGAGGGCTTA 301
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QY 302 -----ATTACGGGGGCTTATTGGGGCCAAAGGACACAGGTCACCGTCTCTCCTGAGGTGAG 355
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Db 302 CTATGTCTTACTTTTACTACTGTGGGCCAAAGTACACAGGTCAACCGTCTCTCCTGAGGTGAG 361
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QY 356 GCGGCTCAGGCGGAGGTGCTGTGGCGGTGGCGGATCGACATTTGACTCAACCCAGTCTC 415
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Db 362 GCGGTTCAAGCGGAGTTGGCTCTGGCGGTGGCGGATCGACATTCGAGCTCACTCAGTCTC 421
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QY 416 CAGCAATCATGTCTGATCTCCAGGGGAGAGGCTCACATGACTGTGCAAGTCCAGTTCAA 475
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Db 422 CAGCAATCATGTCTGATCTCCAGGGGAGAGGCTCACATGACTGTGCAAGTCCAGTCTCAA 481
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QY 476 GTGTAAAGTACATGAAGCTGTTCCAAAGAGTACAGGACCTCCCAAGAGTGGATT 535
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Db 482 GTATTAAGTTACATGACTGTGTATCAGCAAGAGCCAGGACCTCCCAAGAGTGGATT 541
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QY 536 ATGACACATCCAAACTGTCTTGTGAGTCCCTGCTCTGCTTCAAGTGGAGTGGGCTGAGGA 595
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Db 542 ATGACACATCCAAACTGTCTTGTGAGTCCCTGCTCTGCTTCAAGTGGAGTGGGCTGAGGA 601
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QY 596 CCTTTACTCTCTCACAATCAGCAGCATGAGGCTGAGAGTGTGCTGCACTTACTGTGCC 655
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Db 602 CCTTTACTCTCTCACAATCAGCAGCATGAGGCTGAGAGTGTGCTGCACTTACTGTGCC 661
|||
QY 656 AGCAGTGAAGTGAACCACTCAGTCTGGGTGCTGGGACCAAGCTGGAGCTGAAA 711
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Db 662 ATCAGCGAGTAGTGAACCACTCAGTCTGGGTGCTGGGACCAAGCTGGAGTAAA 717
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RESULT 12  
US-10-749-522-5

Sequence 5, Application US/10749522  
Publication No. US20050089510A1

GENERAL INFORMATION:

APPLICANT: SOLOMON, Beke

APPLICANT: HANNAN, Elia

TITLE OF INVENTION: AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN DIAG

TITLE OF INVENTION: AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES

FILE REFERENCE: SOLOMON=2B

CURRENT APPLICATION NUMBER: US/10/749,522

PRIOR FILING DATE: 2004-01-02

PRIOR APPLICATION NUMBER: US/09/529,971

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 09/473,653

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: US 60/152,417

PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 29

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5

LENGTH: 717

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(717)

US-10-749-522-5

Query Match	46.5%	Score 442;	DB 21;	Length 717;
Best Local Similarity	77.4%	Pred. No. 1.6e-125;		
Matches 554;	Conservative 0;	Mismatches 150;	Indels 12;	Gaps 1;

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QY 8 AGGTCAAGCTGACGAGAGTCAAGGGGAGGCTTAGTGCACCTGAGAGGATCCCGAAGACTCT 67
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Db 2 AGGTCAAGCTGACGAGAGTCAAGGGGAGGCTTAGTGCACCTGAGAGGATCCCGAAGACTCT 61
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QY 68 CCTGTGACGCTCTGTGATTCACTTTGAGTAGCTTTGGAAATGCACTGGGTTCTGACGGCTC 127
|||
Db 62 CCTGCAAGGGTTCTGTGCTACACATTTACGATTTATGCTATGCACTGGGTAAGACAGAGTC 121
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QY 128 CAGAGAAAGGGGCTGAGGGTGTGCAATATATTAGTAGTGGAGTAGTACCATCTACTATG 187
|||
Db 122 ATGCAAAAGAGTGTAGAGTGTGATTTAGTTATTTAGTTACTATGATGTAGTACTATACA 181
|||
QY 188 CAGACACAGTGAAGGAGATTCACATCTCCAGAGACAATCCCAAGAACACCTGTTCC 247
|||
Db 182 ACCAGAAAGTTCAAGGCAAGGCCACATGACTGTAGACAAATCTCCACACAGCTTATA 241
|||
QY 248 TGCAAATGACAGTCTAAGTCTGAGAGACACCGTCTATTTACTGTGCAAGAG----- 301
|||
Db 242 TGGAACTTGCACAGACTGACATCTGAGAGATTCTGCCATCTATTTACTGTGCAAGAGGGCTTA 301
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QY 302 -----ATTACGGGGGCTTATTGGGGCCAAAGGACCAAGGTCACCGTCTCTCCTGAGGTGAG 355
|||
Db 302 CTATGTCTTACTTTTACTACTGTGGGCCAAAGTACACAGGTCAACCGTCTCTCCTGAGGTGAG 361
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QY 356 GCGGCTCAGGCGGAGGTGCTGTGGCGGTGGCGGATCGACATTTGACTCAACCCAGTCTC 415
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Db 362 GCGGTTCAAGCGGAGTTGGCTCTGGCGGTGGCGGATCGACATTCGAGCTCACTCAGTCTC 421
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QY 416 CAGCAATCATGTCTGATCTCCAGGGGAGAGGCTCACATGACTGTGCAAGTCCAGTTCAA 475
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Db 422 CAGCAATCATGTCTGATCTCCAGGGGAGAGGCTCACATGACTGTGCAAGTCCAGTCTCAA 481
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QY 476 GTGTAAAGTACATGAAGCTGTTCCAAAGAGTACAGGACCTCCCAAGAGTGGATT 535
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Db 482 GTATTAAGTTACATGACTGTGTATCAGCAAGAGCCAGGACCTCCCAAGAGTGGATT 541
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QY 536 ATGACACATCCAAACTGTCTTGTGAGTCCCTGCTCTGCTTCAAGTGGAGTGGGCTGAGGA 595
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Db 542 ATGACACATCCAAACTGTCTTGTGAGTCCCTGCTCTGCTTCAAGTGGAGTGGGCTGAGGA 601
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QY 596 CCTTTACTCTCTCACAATCAGCAGCATGAGGCTGAGAGTGTGCTGCACTTACTGTGCC 655
|||
Db 602 CCTTTACTCTCTCACAATCAGCAGCATGAGGCTGAGAGTGTGCTGCACTTACTGTGCC 661
|||
QY 656 AGCAGTGAAGTGAACCACTCAGTCTGGGTGCTGGGACCAAGCTGGAGCTGAAA 711
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Db 662 ATCAGCGAGTAGTGAACCACTCAGTCTGGGTGCTGGGACCAAGCTGGAGTAAA 717
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RESULT 13

US-09-976-787-30

Sequence 30, Application US/09976787

Patent No. US20020064528A1

GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping

APPLICANT: Witte, Larry

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245/46505

CURRENT APPLICATION NUMBER: US/09/976,787

PRIOR FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 09/493,539

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 30

LENGTH: 720  
 TYPE: DNA  
 ORGANISM: Mouse  
 US-09-976-787-30

Query Match 46.1%; Score 438.2; DB 9; Length 720;  
 Best Local Similarity 76.8%; Pred. No. 2.4e-124;  
 Matches 552; Conservative 0; Mismatches 158; Indels 9; Gaps 1;

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QY 8 AGGTCAAGTGCAGAGTCAAGGGGAGGCTTGTGAGGCTGGAGGGTCCCGAACTCT 67
DB 2 AGGTCAAGTGCAGAGTCTGGGGAGAGCTTGTGGGGTCAAGGGGCTTCACTCAATTGT 61
QY 68 CCTGTGACAGCTCTGTGATTCATCTTTCAGTGTGAAATGCACTGGGTTCTGACGGCTC 127
DB 62 CCGACCAACTCTTGGCTTCAACATTAAGACTTATATGACCTGGGTAAGACAGAGG 121
QY 128 CAGAGAGGGGCTGAGTGGGTGCAATATTAATTAATGAGTGGCACTAGTACTACTATG 187
DB 122 CTGAACAGGGGCTGAGTGGATTTGATGATGATCTGGAATGGTGAATTCGTTATG 181
QY 188 CAGACACAGTGAAGGAGCATTTCACATCTCCAGAGCAATCCCAAGAACACCTGTTC 247
DB 182 CCGGAAAGTTCAGGGGCAAGGCCACATGACATGACATCTCCTCAACAGCCTACC 241
QY 248 TCGCAATGACCAAGTCTAAGGCTGAGGACACGGTCACTGATTTACTGT-----GCAA 298
DB 242 TCGAGCTCAGCAGCTGACATCTGAGGACACTGCCCTTATTAATGATGATCTATG 301
QY 299 GAGATTAGGGGGCTTATTTGGGGCCAAAGGACACGGTCACTGCTCTTCAGGTGAGGG 358
DB 302 GTGACTACGAAGGCTACTGGGGCCAAAGGACACGGTCACTGCTCTTCAGGTGAGGG 361
QY 359 GCTCAGGCGGAGTGGCTCTGGGGGTGGGAGATCGGACATGAGCTCAACCCAGTCTCCAG 418
DB 362 GTTCAGGCGGAGTGGCTCTGGGGGTGGGAGATCGGACATGAGCTCACTCACTCTCCAG 421
QY 419 CAATCATGCTGTCATCTCCAGGGGAGAGGGTCACTGACCTGACAGTGCAGTTCAAGTG 478
DB 422 CAATCATGCTGTCATCTCCAGGGGAGAGGGTCACTGACCTGACAGTGCAGTCAAGTG 481
QY 479 TAAGGATCATGAATGCTGTTCCAAAGAGTCAAGGCACTTCCCAAAAGTGAATTTATG 538
DB 482 TAAGTATCATGACCTGTTCCAGCAGAGCAAGGCACTTCTCCAAAGTGAATTTATA 541
QY 539 ACACATCCAACTGTCTTCTGAGTCCCTGCTGCTTCACTGAGTGGGTCTGGGAACT 598
DB 542 GCACATCCAACTGCTGCTTCTGAGTCCCTGCTGCTTCACTGAGTGGGTCTGGGAACT 601
QY 599 CTACTCTCTCACAATCAGAGCATGAGGCTGAAGATGCTGCACCTTACTACTGCAGC 658
DB 602 CTACTCTCTCACAATCAGAGCATGAGGCTGAAGATGCTGCACCTTACTACTGCAGC 661
QY 659 AGTGAAGTGAATCCCACTCAAGTTCGCTGCTGGGACCAAGCTGAGCTGAACCGGCG 717
DB 662 AAGGAGTGAATCCCACTTCAAGTTCGCTGCTGGGACCAAGCTGAGTGAATTAACCGGCG 720

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RESULT 14  
 US-10-247-488-3  
 Sequence 3, Application US/10247488  
 Publication No. US2003002244A1  
 GENERAL INFORMATION:  
 APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &  
 TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53  
 FILE REFERENCE: 1196336-RAMOT  
 CURRENT APPLICATION NUMBER: US/10/247,488  
 CURRENT FILING DATE: 2002-09-20  
 PRIOR APPLICATION NUMBER: US/09/526,738  
 PRIOR FILING DATE: 2000-03-16  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3

LENGTH: 780  
 TYPE: DNA  
 ORGANISM: Humanus  
 US-10-247-488-3

Query Match 45.8%; Score 436; DB 14; Length 780;  
 Best Local Similarity 75.9%; Pred. No. 1.2e-123;  
 Matches 554; Conservative 0; Mismatches 170; Indels 6; Gaps 1;

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QY 1 ATGGCCAGAGTCAAGTGCAGAGGAGGAGGCTTGTGAGGCTGGAGGGTCCCG 60
DB 1 ATGGCCAGAGTCAAGTGCAGAGGAGGAGGCTTGTGAGGCTGGAGGGTCCCG 60
QY 61 AAATCTCTCTGTCAGACCTCTGTGATTCATCTTCACTGAGTGTGAAATGCACTGGGTTCT 120
DB 61 AGATGCTCTGCAAGACTTCTGGCTACACTTACTAGCTACATGATGAATGGTAAAA 120
QY 121 CAGGCTCCAGAGAGGGGCTGAGTGGGTGCAATATTAATTAATGAGTGGCACTAGTACTATC 180
DB 121 CAGAGGCTGGAACAGGGTCTGGAATGGATTTGATATTAATCTTACACTGGTTTACT 180
QY 181 TCTATGACAGACAGTGAAGGAGCATTCACATCTCCAGAGCAATCCCAAGAACCC 240
DB 181 AGTATCATGAGAGTTCAGAGCAAGGCCCATTAATGACAGCAAAATCTTCACAGC 240
QY 241 CTGTTCTGCAATGACCAAGTCTAAGTCTGAGGACACGGTCACTGATTTACTGTGCAAG 300
DB 241 GCTTATCATGACCAAGTCTGAGGCTGACCAATGATGACTCTGCACTTATTAATGTA 300
QY 301 GATTAC-----GGGGCTTATTTGGGGCCAAAGGACACGGTCACTGCTCTTCAGGTGA 354
DB 301 GATTACTTATTTATTTACTACTAGGGGCCAAAGGACACGGTCACTGCTCTTCAGGTGA 360
QY 355 GGCGGCTCAGGGGAGAGTGGCTCTGGCGGTGGCGGATCGGACATGAGTCAACCCAGTCT 414
DB 361 GGCGGCTCAGGGGAGAGTGGCTCTGGCGGTGGCGGATCGGACATGAGTCAACCCAGTCT 420
QY 415 CCAGCATATGCTGTCATCTCCAGGGGAGAGGGTCACTGACCTGACCTGCACTGCACTTCA 474
DB 421 CCAGCATATGCTGTCATCTCCAGGGGAGAGGGTCACTGACCTGACCTGCACTGCACTCA 480
QY 475 AGTGAAGTGAATGAGTGTTCACAGAGTCAAGGCACTTCCCAAAAGTGAATTTATG 534
DB 481 AGTGAATTAATTAATGAGTGTTCACAGAGGAGGCACTTCTCCAAAGTGAATTTATG 540
QY 535 TATGAACATCCAACTGTCTTCTGAGTCCCTGCTGCTTCACTGAGTGGGTCTGGG 594
DB 541 TATGAACATCCAACTGTCTTCTGAGTCCCTGCTGCTTCACTGAGTGGGTCTGGG 600
QY 595 ACCTTTACTCTCTCACAATCAGAGCATGAGGCTGAAGATGCTGCCATTTACTACTGC 654
DB 601 ACCTTTACTCTCTCACAATCAGAGCATGAGGCTGAAGATGCTGCCATTTACTACTGC 660
QY 655 CAGCAGTGAAGTGAATCCCACTCAAGTTCGCTGCTGGGACCAAGCTGAGCTGAACCGG 714
DB 661 CAGCAAGGAGTGAATCCCACTCAAGTTCGCTGCTGGGACCAAGCTGAGCTGAACCGG 720
QY 715 GCGGCGCGCAG 724
DB 721 GCGGCGCGCAG 730

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RESULT 15  
 US-08-940-544-3  
 Sequence 3, Application US/08940544B  
 Publication No. US20020018783A1  
 GENERAL INFORMATION:  
 APPLICANT: SADELAINE, MICHEL  
 APPLICANT: CHEUNG, NAI-KONG V.  
 APPLICANT: KRAUSE, ANUA  
 APPLICANT: GUO, HONG-FEN  
 TITLE OF INVENTION: FUSION PROTEINS OF A SINGLE CHAIN ANTIBODY AND CD28 AND  
 TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: MSK-P-035-US  
CURRENT APPLICATION NUMBER: US/08/940,544B  
CURRENT FILING DATE: 1997-09-30  
EARLIER APPLICATION NUMBER: PCT/US97/04427  
EARLIER FILING DATE: 1997-03-20  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 717  
TYPE: DNA  
ORGANISM: HUMAN  
FEATURE:  
OTHER INFORMATION: 5F11-bcfv  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (37)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (79)  
US-08-940-544-3

Query Match 45.7%; Score 434.8; DB 8; Length 717;  
Best Local Similarity 76.5%; Pred. No. 2,6e-123;  
Matches 548; Conservative 0; Mismatches 159; Indels 9; Gaps 1;

QY 8 AGGTCAAGCTGCAAGAGTCAAGGGGAGCTTAGTGCAGCTTGAGGGTCCCGAAACTCT 67  
DB 2 AGGTGAACTGCAGAGCTGAGGACCTGAACTGGTGNAGCTTGAGGCTTCAGTGAAGATAT 61  
QY 68 CCTGTGACAGCTCTGTGATTCACTTTGAGAGCTTTGGAATGCACTGGGGTTGTCAGGGCTC 127  
DB 62 CTTGCAAGACTTCTTGAAACAATTTCTGAATACCAATGCACTGGGTGAAGACAGGCC 121  
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DB 122 ATGGAAGAAGCCTTAGTGGATTGAGGATTTATCTTAACATGGTGGTACTAATCTACA 181  
QY 188 CAGACACACTGAAGGAGCATTTACCATCTCCAGAGACAATCCCAAGAACCCCTGTTCC 247  
DB 182 AGCAGAAATTCAAGGGCAAGGCCACATGTGATGACAAAGTCTCCAGACAGCCTACA 241  
QY 248 TGCATAATGACCACTTAAGSTCTGAGGAGACCGTCACTGATTAATCTGTGCAAGATTACG 307  
DB 242 TGGAGCTCCGACCTGACATCTGAGGATTTGCACTTATTACTGTGCAAGAGATCTA 301  
QY 308 GG-----GCTTATTGGGGCAAGGGACACCGTCAACGCTCTCTCAGGTGAGGCG 358  
DB 302 CGGTCCCGTTTGTCTTACTGGGTCAAGGGACCAAGTCAACGCTCTCTCAGGTGAGGCG 361  
QY 359 GCTCAGGCGGAGGTGCTCTGGGGTGGCGGATCGGACATTGAGCTCACCAAGTCTCAG 418  
DB 362 GTTCAGGCGGAGGTGCTCTGGGGTGGCGGATCGGACATTGAGCTCACCAAGTCTCAG 421  
QY 419 CAATCATGCTGACATCTCAGGGGAGAGGGTCAACATGACCTGACAGTGCAGTTCAAGTG 478  
DB 422 CAATCATGCTGACATCTCAGGGGAGAGGGTCAACATGACCTGACAGTGCAGTTCAAGTA 481  
QY 479 TAAGGTACATGAAGTGTTCACACAGAACTCAGGCACCTCCCCAAAAGATGATTTATG 538  
DB 482 TAAATTACATGACCTGTATCAGCAGAAAGCTGTCACTCCCCAAAAGATGATTTATG 541  
QY 539 ACAACATCCAACTGTCTTCTGAGATCCCTGCTGCTTCAAGTGGCAAGTGGGCTCGGAGCT 598  
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QY 599 CTTACTCTCTCAATCAGCAGATGAGGCTGAAGATGCTGCACCTTACTACTGACAGC 658  
DB 602 CTTATTCTCTCAACATCAGCAGATGAGGCTGTAGATGCTGCACCTTATTTACTGCAATC 661  
QY 659 AGTGAAGTAGTAACCACTCAGCTTGGTGGTGGGACCAAGCTGAGCTGAACGG 714  
DB 662 AGCGAGTAGTAAACCGCTCACGTTGGTGGTGGGACACAGTTGGAATAAAACGG 717

Search completed: June 23, 2005, 12:47:09  
Job time : 691 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 06:39:36 ; Search time 201 Seconds  
(without alignments)  
7741.787 Million cell updates/sec

Title: US-09-403-882a-1

Perfect score: 951  
Sequence: 1 atggccagatcagctgca.....ggcagaagaagccagctag 951

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	749.6	78.8	1256	3 US-09-553-498-7	Sequence 7, Appl1
2	749.6	78.8	1256	3 US-09-518-869-7	Sequence 7, Appl1
3	653.8	68.7	738	2 US-08-956-047-24	Sequence 24, Appl1
4	651	68.5	711	2 US-08-190-199A-64	Sequence 64, Appl1
5	580.6	61.1	672	2 US-08-190-199A-62	Sequence 62, Appl1
6	543.6	57.2	793	2 US-08-956-047-29	Sequence 29, Appl1
7	462.8	48.7	708	2 US-08-190-199A-60	Sequence 60, Appl1
8	462.2	48.6	858	3 US-08-564-164A-1	Sequence 1, Appl1
9	460.2	48.4	807	4 US-09-674-677-4	Sequence 1, Appl1
10	449.6	47.3	1679	3 US-08-661-052-15	Sequence 15, Appl1
11	449.6	47.3	1679	3 US-09-188-082-15	Sequence 15, Appl1
12	449.6	47.3	1679	3 US-09-364-088-15	Sequence 15, Appl1
13	449.6	47.3	1679	3 US-09-102-716-15	Sequence 15, Appl1
14	443.6	46.6	1176	3 US-09-142-974B-3	Sequence 3, Appl1
15	442	46.5	717	4 US-09-473-653-5	Sequence 5, Appl1
16	437.6	46.0	810	4 US-08-652-507-1	Sequence 1, Appl1
17	436	45.8	780	4 US-09-526-738A-3	Sequence 3, Appl1
18	434.8	45.7	717	3 US-09-142-974B-1	Sequence 1, Appl1
19	433.8	45.6	714	4 US-09-798-689-22	Sequence 22, Appl1
20	430.6	45.3	771	4 US-09-526-738A-1	Sequence 1, Appl1
21	417.2	43.9	720	3 US-08-279-772A-7	Sequence 7, Appl1
22	417.2	43.9	720	3 US-08-902-486-10	Sequence 10, Appl1
23	416.8	43.8	883	4 US-09-184-658-7	Sequence 7, Appl1
24	416.8	43.8	883	4 US-09-504-262D-7	Sequence 7, Appl1
25	413.6	43.5	1797	1 US-08-463-163-2	Sequence 2, Appl1
26	411.8	43.3	723	4 US-09-581-345-1	Sequence 1, Appl1
27	409.4	43.0	786	3 US-08-635-928-31	Sequence 31, Appl1

28	407.4	42.8	726	2 US-08-553-497A-25	Sequence 25, Appl1
29	406.6	42.8	924	2 US-08-860-174A-9	Sequence 9, Appl1
30	406.6	42.8	924	3 US-09-171-025-26	Sequence 26, Appl1
31	406.6	42.8	924	4 US-09-742-693-26	Sequence 26, Appl1
32	405.6	42.6	843	3 US-09-423-439-43	Sequence 43, Appl1
33	400.8	42.1	894	4 US-09-486-814A-1	Sequence 1, Appl1
34	400.4	42.1	726	2 US-08-553-497A-27	Sequence 27, Appl1
35	400.4	42.1	1445	2 US-09-948-004-17	Sequence 17, Appl1
36	395.6	41.6	720	4 US-09-192-854-1	Sequence 1, Appl1
37	395.4	41.6	717	2 US-08-553-497A-17	Sequence 17, Appl1
38	394.8	41.5	930	3 US-09-171-025-3	Sequence 3, Appl1
39	392.4	41.3	669	2 US-08-190-199A-66	Sequence 66, Appl1
40	390.8	41.1	732	2 US-08-553-497A-19	Sequence 19, Appl1
41	390.8	41.1	732	2 US-08-553-497A-21	Sequence 21, Appl1
42	388.2	40.8	1398	3 US-09-423-439-50	Sequence 50, Appl1
43	383.6	40.3	907	3 US-09-184-658-9	Sequence 9, Appl1
44	383.6	40.3	907	3 US-09-504-262D-9	Sequence 9, Appl1
45	373.2	39.2	738	2 US-08-553-497A-23	Sequence 23, Appl1

## ALIGNMENTS

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RESULT 1
US-09-553-498-7
; Sequence 7, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted protei
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
; LENGTH: 1256
; TYPE: DNA
; ORGANISM: E. coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)...(969)
US-09-553-498-7
Query Match 78.8%; Score 749.6; DB 3; Length 1256;
Best Local Similarity 98.2%; Pred. No. 2.9e-205;
Matches 758; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1 ATGGCCAGATCAAGCTGCAAGAGTCAAGGGGAGGCTTGTAGTGCAGCTTGAGGCTCCCG 60
DB 199 ATGGCCAGATCAAGCTGCAAGAGTCTGGGGGAGGCTTGTAGTGCAGCTTGAGGCTCCCG 258
QY 61 AAACCTCCGTCGACCTCTGTGATTCACCTTGTAGTGTGGAATGCACTGGTTGCT 120
DB 259 AAACCTCCGTCGACCTCTGTGATTCACCTTGTAGTGTGGAATGCACTGGTTGCT 318
QY 121 CAGGCTCCAGAGAGGGGCTGAGTGGTGCATATATATAGTAGGCAAGTATACATC 180
DB 319 CAGGCTCCAGAGAGGGGCTGAGTGGTGCATATATAGTAGGCAAGTATACATC 378
QY 181 TACTATGCAAGACAGTGAAGGAGCATTCATCTCCAGAGACATCCCAAGAACCC 240
DB 379 TACTATGCAAGACAGTGAAGGAGCATTCATCTCCAGAGACATCCCAAGAACCC 438
QY 241 CTTTCTCTGGAATGACAGTCTAAGCTCTGAGAGACAGGCTATATTAATCTGCAAGA 300
DB 439 CTTTCTCTGGAATGACAGTCTAAGCTCTGAGAGACAGGCTATATTAATCTGCAAGA 498
QY 301 GATTACGGGGCTTATTTGGGGCCCAAGGACACAGGTCTCTCAGGTGAGGCGGC 360
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Db 499 GATTACGGGGCTTATTTGGGGCCAAAGGACCAAGGTCAACGCTCTCCCTCAGGTGAGGCGGT 558  
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Db 559 TCGAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGACATTGAGTCCACCAAGTCTCCAGCA 618  
Qy 421 ATCATGTCTGCATCTTCAGAGGAGAGAGGTCAACATGACCTGCAAGTCCAGTTCAAGTGA 480  
Db 619 ATCATGTCTGCATCTTCAGAGGAGAGAGGTCAACATGACCTGCAAGTCCAGTTCAAGTGA 678  
Qy 481 AGGTACATGAATCTGGTTCCAAAGATGAGGACCTCCCCCAAAAGATGATTTATGAC 540  
Db 679 AGGTACATGAATCTGGTTCCAAAGATGAGGACCTCCCCCAAAAGATGATTTATGAC 738  
Qy 541 ACATCCAAACTGTCTTCTGGAGTCCCTGCTGCTTCAAGTGGAGTGGGTCTGGACCTCT 600  
Db 739 ACATCCAAACTGTCTTCTGGAGTCCCTGCTGCTTCAAGTGGAGTGGGTCTGGACCTCT 798  
Qy 601 TACTCTTCACATCAGCAGCATGAGAGGCTGAAGATGCTGCACCTTACTACTGCCAGCAG 660  
Db 799 TACTCTTCACATCAGCAGCATGAGAGGCTGAAGATGCTGCACCTTACTACTGCCAGCAG 858  
Qy 661 TGGAGTAGTAATCCCACTCACTGCTGGGTGCTGGGACCACTGGAAGTGAAGCGGCGGCT 720  
Db 859 TGGAGTAGTAATCCCACTCACTGCTGGGTGCTGGGACCACTGGAAGTGAAGCGGCGGCT 918  
Qy 721 GCAGAACAAAACATCATCTCAGAGAGATGGAATGGGGCGGTGCAGCAAC 772  
Db 919 GCAGAACAAAACATCATCTCAGAGAGATGGAATGGGGCGGTGCAGTAATGAC 970

## RESULT 2

US-09-618-869-7  
; Sequence 7, Application US/09618869  
; Patent No. 6455279  
; GENERAL INFORMATION:  
; APPLICANT: Ambrosius, Dorthree  
; APPLICANT: Rudolph, Rainer  
; APPLICANT: Schaeffner, Joerg  
; APPLICANT: Schwarz, Elisabeth  
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND  
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR  
; TITLE OF INVENTION: CHAPERONES  
; FILE REFERENCE: 20381  
; CURRENT APPLICATION NUMBER: US/09/618,869  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: EP9114811.5  
; PRIOR FILING DATE: 1999-07-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 1256  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (199)..(969)  
US-09-618-869-7

Query Match 78.8%; Score 749.6; DB 3; Length 1256;  
Best Local Similarity 98.2%; Pred. No. 2,9e-205;  
Matches 758; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGGCGGAGGTGAAGTGCAGAGTCAAGGAGGCTTGTGCAGGCTCGAGAGGTCGCGG 60  
Db 199 ATGGCGGAGGTGAAGTGCAGAGTGTGGGAGGCTTGTGCAGGCTCGAGAGGTCGCGG 258  
Qy 61 AAATCTCTCTGTCAGGCTCTGGATTCATTTCAGTAGCTTTGGAATGATGAGTGGTGGT 120  
Db 259 AAATCTCTCTGTCAGGCTCTGGATTCATTTCAGTAGCTTTGGAATGATGAGTGGTGGT 318  
Qy 121 CAGGCTCCAGAGAGGGGCTGAGTGGGTGCATATATTAGTAGTGGCAGTAGTACCATC 180

Db 319 CAGGCTCCAGAGAGGGGCTGAGTGGGTGCATATATTAGTAGTGGCAGTAGTACCATC 378  
Qy 181 TACTATGACAGACAGTAGAAGGAGCATTTCAACATCTCCAGAGACATATCCCAAGAACAC 240  
Db 379 TACTATGACAGACAGTAGAAGGAGCATTTCAACATCTCCAGAGACATATCCCAAGAACAC 438  
Qy 241 CTGTTCTTCGAAATGACAGTCTAAGGTCTGAGGACACAGGTCTATGATTTACTGTCAGAA 300  
Db 439 CTGTTCTTCGAAATGACAGTCTAAGGTCTGAGGACACAGGTCTATGATTTACTGTCAGAA 498  
Qy 301 GATTACGGGGCTTATTTGGGGCCCAAGGACCAAGTCAACCTTCTCTCAGGTGGAGCGGCT 360  
Db 499 GATTACGGGGCTTATTTGGGGCCCAAGGACCAAGTCAACCTTCTCTCAGGTGGAGCGGCT 558  
Qy 361 TCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGACATTTGAGTCAACCAAGTCTCCAGCA 420  
Db 559 TCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGACATTTGAGTCAACCAAGTCTCCAGCA 618  
Qy 421 ATCATGTCTGCATCTTCAGAGGAGAGGCTCAACATGACCTGCAAGTCCAGTTCAAGTGA 480  
Db 619 ATCATGTCTGCATCTTCAGAGGAGAGGCTCAACATGACCTGCAAGTCCAGTTCAAGTGA 678  
Qy 481 AGGTACATGAATCTGGTTCCAAAGATGAGGACCTCCCCCAAAAGATGATTTATGAC 540  
Db 679 AGGTACATGAATCTGGTTCCAAAGATGAGGACCTCCCCCAAAAGATGATTTATGAC 738  
Qy 541 ACATCCAAACTGTCTTCTGGAGTCCCTGCTGCTTCAAGTGGAGTGGGTCTGGACCTCT 600  
Db 739 ACATCCAAACTGTCTTCTGGAGTCCCTGCTGCTTCAAGTGGAGTGGGTCTGGACCTCT 798  
Qy 601 TACTCTTCACATCAGCAGCATGAGAGGCTGAAGTGTCTGCACCTTACTACTGCCAGCAG 660  
Db 799 TACTCTTCACATCAGCAGCATGAGAGGCTGAAGTGTCTGCACCTTACTACTGCCAGCAG 858  
Qy 661 TGGAGTAGTAATCCCACTCACTGCTGGGTGCTGGGACCACTGGAAGTGAAGCGGCGGCT 720  
Db 859 TGGAGTAGTAATCCCACTCACTGCTGGGTGCTGGGACCACTGGAAGTGAAGCGGCGGCT 918  
Qy 721 GCAGAACAAAACATCATCTCAGAGAGATGGAATGGGGCGGTGCAGCAAC 772  
Db 919 GCAGAACAAAACATCATCTCAGAGAGATGGAATGGGGCGGTGCAGTAATGAC 970

## RESULT 3

US-08-956-047-24  
; Sequence 24, Application US/08956047  
; Patent No. 5882924  
; GENERAL INFORMATION:  
; APPLICANT: Fritz, Hans-Joachim  
; APPLICANT: Hennecke, Frank  
; APPLICANT: Kolmar, Harald  
; TITLE OF INVENTION: Genetic Selection, by Means of Signal  
; TITLE OF INVENTION: Transduction in Microorganisms, of Proteins which are  
; TITLE OF INVENTION: Capable of Ligand Binding  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farbow, Garrett & Dunner  
; STREET: 1300 I Street, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.

; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/956,047  
; FILING DATE: 22-OCT-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:



APPLICATION NUMBER: US 08/257,669  
 FILING DATE: 08-JUN-1994  
 APPLICATION NUMBER: DE P 43 19 296.3  
 FILING DATE: 10-JUN-1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pohlman, Sandra M.  
 REGISTRATION NUMBER: P39,691  
 REFERENCE/DOCKET NUMBER: 05552.1368-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 738 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..720  
 OTHER INFORMATION: /note="Molecule 1-720 encodes a  
 OTHER INFORMATION: peptide."  
 US-08-956-047-24

Query Match 68.7%; Score 653.8; DB 2; Length 738;  
 Best Local Similarity 94.8%; Pred. No. 7.9e-178;  
 Matches 676; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

2 TGGCCGAGGTCAAGCTGCAAGAGTCAAGGGGAGGCTTAAAGTCAGAGCTGAGGGTCCCGA 61  
 8 TGCATACGTAACGTCAGCTGCTGAGAGCTTGGGGAGGCTTTGGTCAGAGCTGAGGGTCCCGA 67  
 62 AACTCTCTGTCAGAGCTCTGCAATTCATCTTCACTTCACTTCACTTCACTTCACTTCACTT 121  
 68 AACTCTCTGTCAGAGCTCTGCAATTCATCTTCACTTCACTTCACTTCACTTCACTTCACTT 127  
 122 AGGCTCAGAGAGGGGCTGAGTGGGTGATATATTAGTAGGAGAGTACATCT 181  
 128 AGGCTCAGAGAGGGGCTGAGTGGGTGATATATTAGTAGGAGAGTACATCT 187  
 182 ACTATCAGACACAGTGAAGGAGCGATTCACTTCCAGAGCAATCCCAAGAACCC 241  
 188 ACTATCAGACACAGTGAAGGAGCGATTCACTTCCAGAGCAATCCCAAGAACCC 247  
 242 TGTTCCTGCAATGACCACTGTAAGTCTGAGAGCAAGGCTCATGTAATTAAGTCTGCAAG 301  
 248 TGTTCCTGCAATGACCACTGTAAGTCTGAGAGCAAGGCTCATGTAATTAAGTCTGCAAG 307  
 302 ATTACGGGGCTTATTTGGGGCCAGAGGACACGGTCAACCGTCTGCTCAGAGTGGAGGGGCT 361  
 308 ATTACGGGGCTTATTTGGGGCCAGAGGACACCGTCTGCTCAGAGTGGAGGGGCT 367  
 362 CAGGCGAGGTGCTCTGCGGTGCGGATCGAGCAATTGAGCTCACCAGTCTCCAGCA 421  
 368 CAGGCGAGGTGCTCTGCGGTGCGGATCGGCAATTTGTTCTCACCCAGTCTCCAGCA 427  
 422 TCATGTCGATCTCCAGGGGAGAGGCTACCATGACCTGACAGTCCAGTCAAGTGTAA 481  
 428 TCATGTCGATCTCCAGGGGAGAGGCTACCATGACCTGACAGTCCAGTCAAGTGTAA 487  
 482 GGTACATGAATGATGTTCCACAGAGTCAAGGACCTCCCAAGAGCTGACATATGACA 541  
 488 GGTACATGAATGATGTTCCACAGAGTCAAGGACCTCCCAAGAGCTGACATATGACA 547  
 542 CATCAAACTGCTTCTGAGATCCCTGCTGCTTCACTGAGTGGAGTGGAGCTCTT 601  
 548 CATCAAACTGCTTCTGAGATCCCTGCTGCTTCACTGAGTGGAGTGGAGCTCTT 607  
 602 ACTCTCTCACAATCAGACGATGAGGCTGAAGATGCTGCACCTTACTTACTGCCAGAGT 661  
 608 ACTCTCTCACAATCAGACGATGAGGCTGAAGATGCTGCACCTTACTTACTGCCAGAGT 667

QY 662 GGAGTAGTAACCACTACAGTTGCTGCGGACCAAGCTGAGCTGAACCG 714  
 DB 668 GGAGTAGTAACCACTACAGTTGCTGCGGACCAAGCTGAGCTGAACCG 720

RESULT 4  
 US-08-190-199A-64  
 Sequence 64, Application US/08190199A  
 Patent No. 5830663

GENERAL INFORMATION:  
 APPLICANT: EMBLETON, Michael J.  
 APPLICANT: GOROCHEV, Guy  
 APPLICANT: JONES, Peter T.  
 APPLICANT: WINTER, Gregory P.  
 TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS  
 NUMBER OF SEQUENCES: 70  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005-3918

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/190,199A  
 FILING DATE: 13-JUL-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB92/01483  
 FILING DATE: 10-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9212419.7  
 FILING DATE: 11-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9117352.6  
 FILING DATE: 10-AUG-1991

INFORMATION FOR SEQ ID NO: 64:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 711 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..708  
 US-08-190-199A-64

Query Match 68.5%; Score 651; DB 2; Length 711;  
 Best Local Similarity 95.0%; Pred. No. 4.9e-177;  
 Matches 672; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

7 GAGGTCAAGCTGACAGATCAGAGGAGGCTTATGTCAGGCTGAGAGGCTCCGAAATCTC 66  
 1 GAGGTCAAGCTGACAGATCAGAGGAGGCTTATGTCAGGCTGAGAGGCTCCGAAATCTC 60  
 67 TCTGTGACAGCTCTGGAATTCATTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 126  
 61 TCTGTGACAGCTCTGGAATTCATTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 120  
 127 CCAGAGAGGGGCTGAGTGGGTGCGATATATTAGTAGGAGGAGTGAATCATCTACTAT 186  
 121 CCAGAGAGGGGCTGAGTGGGTGCGATATATTAGTAGGAGGAGTGAATCATCTACTAT 180  
 187 GCAGACACAGTGAAGGAGGATTCACCATCTCCAGAGCAATCCCAAGAACCTGTTTC 246

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Db      181 GGAGACACAGTAAAGGGCCGATTCACATCTCCAGAGCAATCCCAAGAACCCCTGTTAC 240
Qy      247 CTGCAAAATGACAGCTTAAGTCTGAGAGACAGGTCATGATTTACTGTCAGAGATTAC 306
Db      241 CTGCAAAATGACAGCTTAAGTCTGAGAGACAGGTCATGATTTACTGTCAGAGATTAC 300
Qy      307 GGGGCTTATTTGGGCGCAAGGAGCAACGCTCACCCTGCTCCAGTGGAGCGGCTCAGGC 366
Db      301 GGGGCTTATTTGGGCGCAAGGAGCACTGCTCAGCTGCTGCAAGTGGTGGTGGTGGT 360
Qy      367 GGAGGTGCTCTGGCGGTGGCGGATTCGATTCAGTCACTCCAGTCTCCAGATTCATC 426
Db      361 GGTCGCGCAAGTGGCGGCGGCTCTCAATTTGTTCTAACCCAGTCTCCAGATTCATC 420
Qy      427 TCTGCATCTCCAGGGGAGAGGTCACCATGACCTGCGAGTGCAGTTCAAGTGAAGTAC 486
Db      421 TCTGCATCTCCAGGGGAGAGGTCACCATGACCTGCGAGTGCAGTTCAAGTGAAGTAC 480
Qy      487 ATGAACCTGTTCCAAACAGAGTCAGGCACTCCCTCCCAAAAGATGATTTATGACATCC 546
Db      481 ATGAACCTGTTCCAAACAGAGTCAGGCACTCCCTCCCAAAAGATGATTTATGACATCC 540
Qy      547 AAACGTCTCTTGGAGTCCCTGCTGCTCAGTGGAGAGTGGTCTGGGACCTTTACTCT 606
Db      541 AAACGTCTCTTGGAGTCCCTGCTGCTCAGTGGAGAGTGGTCTGGGACCTTTACTCT 600
Qy      607 CTCACATCAGCAGCATGAGGCTGAGAGTGTGCTGACCTTACTACTGTCAGAGTGAAT 666
Db      601 CTCACATCAGCAGCATGAGGCTGAGAGTGTGCTGACCTTACTACTGTCAGAGTGAAT 660
Qy      667 AGTAAACCACTCAGCTTGGTGGTGGGACCAAGCTGAGCTGAACG 713
Db      661 AGTAAATCCACTCAGCTTGGTGGGACCAAGCTGAGCTGAACG 707

RESULT 5
US-08-190-199A-62
; Sequence 62, Application US/08190199A
; Patent No. 5830663
; GENERAL INFORMATION:
; APPLICANT: EMBLETON, Michael J.
; APPLICANT: GOROCHOV, Guy
; APPLICANT: JONES, Peter T.
; APPLICANT: WINTER, Gregory P.
; TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,199A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01483
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9212419.7
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9117352.6
; FILING DATE: 10-AUG-1991
; INFORMATION FOR SEQ ID NO: 62:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 672 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..669
; US-08-190-199A-62

Query Match      61.1%; Score 580.6; DB 2; Length 672;
Best Local Similarity 91.1%; Pred. No. 8.3e-157;
Matches 644; Conservative 0; Mismatches 24; Indels 39; Gaps 1;

Qy      7 GAGGTCAAGCTGCAAGAGTCAAGGGAGGCTTAAGTCAGAGCTTGGAGGCTCCCGAAATC 66
Db      1 GATGTGACAGCTGTGGAGTCTGGGGAGGCTTAAGTCAGAGCTTGGAGGCTCCCGAAATC 60
Qy      67 TCTGTGAGAGCTCTGATTAATCACTTTCAGTAGCTTTGGAATGCACTGGGTTGTCAGGCT 126
Db      61 TCTGTGAGAGCTCTGATTAATCACTTTCAGTAGCTTTGGAATGCACTGGGTTGTCAGGCT 120
Qy      127 CCAGAGAGGGGCTGAGTGGGTCGATATATTAAGTAGTGGCAGTAGTACATCTACTAT 186
Db      121 CCAGAGAGGGGCTGAGTGGGTCGATATATTAAGTAGTGGCAGTAGTACATCTACTAT 180
Qy      187 GCAGACAGTGAAGAGGACATTCACCATCTCCAGAGCAATCCCAAGAACCTCTGTTTC 246
Db      181 GCAGACAGTGAAGAGGACATTCACCATCTCCAGAGCAATCCCAAGAACCTCTGTTTC 240
Qy      247 CTGCAATAGACAGCTTAAGTCTGAGAGCAAGGTCATGTATTAAGTGAAGATTAC 306
Db      241 CTGCAATAGACAGCTTAAGTCTGAGAGCAAGGTCATGTATTAAGTGAAGATTAC 300
Qy      307 GGGGCTTATTTGGGCGCAAGGAGCAACGCTCACCGTCTCAGTGGAGCGGCTCAGGC 366
Db      301 GGGGCTTATTTGGGCGCAAGGAGCAACGCTCACCGTCTCAGTGGAGCGGCTCAGGC 360
Qy      367 GGAGTGGCTCTGGCGGTGGCGGATTCGACATTAAGTCACTCCAGTCTCCAGATTCATC 426
Db      348 -----CCAAATTTGTTCCACCAATCTCCAGCAATTCATG 381
Qy      427 TCTGCATCTCCAGGGGAGAGGTCACATGACCTGACAGTTCAGTTCAAGTGAAGTAC 486
Db      382 TCTGCATCTCCAGGGGAGAGGTCACATGACCTGACAGTTCAGTTCAAGTGAAGTAC 441
Qy      487 ATGAACCTGTTCCAAACAGAGTCAGGCACTCCCTCCCAAAAGATGATTTATGACATCC 546
Db      442 ATGAACCTGTTCCAAACAGAGTCAGGCACTCCCTCCCAAAAGATGATTTATGACATCC 501
Qy      547 AAACGTCTCTTGGAGTCCCTGCTGCTCAGTGGAGAGTGGTCTGGGACCTTTACTCT 606
Db      502 AAACGTCTCTTGGAGTCCCTGCTGCTCAGTGGAGAGTGGTCTGGGACCTTTACTCT 561
Qy      607 CTCACATCAGCAGCATGAGGCTGAAGATCTGCACTTAAGTCTGTCAGAGTGAAGT 666
Db      562 CTCACATCAGCAGCATGAGGCTGAAGATCTGCACTTAAGTCTGTCAGAGTGAAGT 621
Qy      667 AGTAAACCACTCAGCTTGGTGGTGGGACCAAGCTGAGCTGAACG 713
Db      622 AGTAAATCCACTCAGCTTGGTGGGACCAAGCTGAGCTGAACG 668

RESULT 6
US-08-956-047-29
; Sequence 29, Application US/08956047
; Patent No. 5882924
; GENERAL INFORMATION:
; APPLICANT: Pritz, Hans-Joachim
; APPLICANT: Hennecke, Frank

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1  APPLICANT: Kolmar, Harold
2  TITLE OF INVENTION: Genetic Selection, by Means of Signal
3  TITLE OF INVENTION: Transduction in Microorganisms, of Proteins which are
4  TITLE OF INVENTION: Capable of Ligand Binding
5  NUMBER OF SEQUENCES: 45
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett & Dunner
8  STREET: 1300 I Street, N.W., Suite 600
9  CITY: Washington
10 STATE: D.C.
11 COUNTRY: USA
12 ZIP: 20005-3315
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent In Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/956,047
20 FILING DATE: 22-OCT-1997
21 CLASSIFICATION: 435
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/257,669
24 FILING DATE: 08-JUN-1994
25 APPLICATION NUMBER: DE P 43 19 296.3
26 FILING DATE: 10-JUN-1993
27 CLASSIFICATION: 435
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Pohlman, Sandra M.
30 REGISTRATION NUMBER: P39,691
31 REFERENCE/DOCKET NUMBER: 05552.1368-00000
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 202-408-4000
34 TELEFAX: 202-408-4400
35 INFORMATION FOR SEQ ID NO: 29:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 793 base pairs
38 TYPE: nucleic acid
39 STRANDEDNESS: double
40 TOPOLOGY: linear
41 MOLECULE TYPE: DNA (genomic)
42 FEATURE:
43 NAME/KEY: CDS
44 LOCATION: 16..354
45 OTHER INFORMATION: /note= "Molecules 16-354 encode a
46 OTHER INFORMATION: peptide."
47 FEATURE:
48 NAME/KEY: CDS
49 LOCATION: 383..775
50 OTHER INFORMATION: /note= "Molecules 383-775 encode a
51 OTHER INFORMATION: peptide."
52 US-08-956-047-29

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	Query Match	Similarity	Score	DB 2	Length
	Best Local	85.2%	Pred. No. 3,9e-146		
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Db	8	TGCAGTACGTACAGCTGTGTGGAGCTTGGGGGAGGCTTTGTGACGCTGAGAGGGTCCGGA	67		
QY	62	AACCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAGCTTTGGATGTGACGTGGGTTCCGTC	121		
Db	68	AACCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAGCTTTGGAAATGACATGGGTTCCGTC	127		
QY	122	AGGCTCCAGAGAGGGGCTGTGAGTGGGTGCGATATATTAGTAGTGGCAGTAGTACATCT	181		
Db	128	AGGCTCCAGAGAGGGGCTGTGAGTGGGTGCGATATATTAGTAGTGGCAGTAGTACATCT	187		
QY	182	ACTATGACAGACACAGTGAAGGAGCATTCACATCTCCAGAGACAAATCCCAAGAACACCC	241		
Db	188	ACTATGACAGACACAGTGAAGGAGCATTCACATCTCCAGAGACAAATCCCAAGAACACCC	247		

Qy	242	TGTTCCGGAATGACCAAGTCTAAGGTTGAGACAAGGTCATATTAATTCGTGCAAGG	301
Db	248	TGTTCCGGAATGACCAAGTCTAAGGTTGAGACAAGGTCATATTAATTCGTGCAAGG	307
Qy	302	ATTACGGGGCTTATTGGGGCCAAAGGACCAAGTCACCGTCTCCTCAAGTGGAGCG---	358
Db	308	ATTACGGGGCTTATTGGGGCCAAAGGACCGTGTCAACGTCTCCTCAAGTAATTCGAAT	367
Qy	359	-----GCTCAGCGGAGGTGGCT	376
Db	368	TCATTTGTACATGAGAAATTAAGTAAACAAGACATAATGCACTGGCACTTTAACG	427
Qy	377	CTGGCGGTGGCGGATTCGAC-----ATTAGCTCAACCGAGTCTCAGCAATATG	426
Db	428	TTACGTGTTACCCCTGTGACAAAACCCCAAAATTTGTCTCACCCAGTCTCCAGCAATATG	487
Qy	427	TCGCACTCCACAGGGGAGGGGTCAACATGACTCGAGTGCAGATTCAGATGTAAGTAC	486
Db	488	TTCGACTTCCAGGGGAGGAAGTCAACATGACTCGAGTGCAGATTCAGATGTAAGTAC	547
Qy	487	ATGAACTGGTTCACACAGAGTCAGAGCACTCCCCAAAAGATGATTTATGACATCC	546
Db	548	ATGAACTGGTTCACACAGAGTCAGAGCACTCCCCAAAAGGTGGAATATGACATCC	607
Qy	547	AAACTGTCTTGTGAGTCCCTGTCTGCTTCAATGAGCAATGGGTTCTGGAACTCTTACTT	606
Db	608	AAACTGTCTTGTGAGTCCCTGTCTGCTTCAATGAGCAATGGGTTCTGGAACTCTTACTT	667
Qy	607	CTCACAATAGACGATGGAAGGTGGAATATGCTGCCATTACTCTGCCAGCAATGAGT	666
Db	668	CTCACAATAGACGATGGAAGGTGGAATATGCTGCCATTACTCTGCCAGCAATGAGT	727
Qy	667	AGTAACCACTCAGCGTGGGTCTGGAGCAAGCTGAGCTGAACGG	714
Db	728	AGTAATCACTCACTTGGGTCTGGAGCAAGCTGAATGAACGG	775

1 RESULT 7  
 2 US-08-190-199A-60  
 3 Sequence 60, Application US/08190199A  
 4 Patent No. 5830663  
 5  
 6 GENERAL INFORMATION:  
 7 APPLICANT: EMBLETON, Michael J.  
 8 APPLICANT: GOROCHOV, Guy  
 9 APPLICANT: JONES, Peter T.  
 10 APPLICANT: WINTER, Gregory P.  
 11 TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS  
 12  
 13 NUMBER OF SEQUENCES: 70  
 14  
 15 CORRESPONDENCE ADDRESS:  
 16 ADDRESSEE: PILSBURY MADISON & SUTRO, L.L.P.  
 17 STREET: 1100 New York Avenue, N.W.  
 18 CITY: Washington  
 19  
 20 STATE: D.C.  
 21  
 22 COUNTRY: U.S.A.  
 23  
 24 ZIP: 20005-3918  
 25  
 26 COMPUTER READABLE FORM:  
 27 MEDIUM TYPE: Floppy disk  
 28 COMPUTER: IBM PC compatible  
 29 OPERATING SYSTEM: PC-DOS/MS-DOS  
 30 SOFTWARE: Microsoft Word  
 31  
 32 CURRENT APPLICATION DATA:  
 33 APPLICATION NUMBER: US/08/190,199A  
 34 FILING DATE: 13-JUL-1994  
 35  
 36 CLASSIFICATION: 435  
 37  
 38 PRIOR APPLICATION DATA:  
 39 APPLICATION NUMBER: PCT/GB92/01483  
 40 FILING DATE: 10-AUG-1992  
 41  
 42 PRIOR APPLICATION DATA:  
 43 APPLICATION NUMBER: GB 9212419.7  
 44 FILING DATE: 11-JUN-1992  
 45  
 46 PRIOR APPLICATION DATA:  
 47 APPLICATION NUMBER: GB 9117352.6  
 48 FILING DATE: 10-AUG-1991

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; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 708 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
US-08-190-199A-60

Query Match      48.7%; Score 462.8; DB 2; Length 708;
Best Local Similarity 79.5%; Pred. No. 6.3e-123;
Matches 561; Conservative 0; Mismatches 142; Indels 3; Gaps 1;

QY 8 AGGTCAAGCTGACGAGGTGAGGGGAGGCTTAGTGCAGCTGAGAGGTCCCGAAACTCT 67
DB 2 AGGTGACGCTGAAGAGGTGACGAGCTGAGCTGGTGGGCTTCACAGAGCTGTCCATCA 61
QY 68 CCTGTGACAGCTCTGGATTCACTTTCAGTGGCTTTGGAATGCACTGGGTTGCTCAGGCTC 127
DB 62 CTTCGACTGTCTCTGGGTTTTCATTACCAAGCTATGTTAACACTGGTTCGCCAGCTTC 121
QY 128 CAGAGAAAGGGGCTGAGTGGTGGCATATATTAGTAGTGGCAGTAGTACATCTATATG 187
DB 122 CAGGAAAGGGGCTGGAGTGGTGGAGTATATGGGCTGTGGAGCAAAATTATATTT 181
QY 188 CAGACACACTGAAGGAGCATTCACCATCTCCAGAGCAATCCCAAGAACACCCTGTTCC 247
DB 182 CGG---CTCTCATATGCCAGACTGAGCATGAGCAAAACAATCCCAAGACCAAGTTTCT 238
QY 248 TGCAAATGACCACTGAAGTCTAGAGACAGCGTCACTGATTACTGTGCAAGAGATTACG 307
DB 239 TAAAATGAAAGTCTGCAAACTGATGACACAGCCATGACTACTGTGCCAAGATCGGG 298
QY 308 GGGCTTATTTGGGGCCCAAGGGACCAAGGTACCGTCTCTCAGGTGAGGGGCTCAGGCG 367
DB 299 GGGCTTATTTGGGGCCCAAGGGACCTGTGTCATCTCTCAGAGTGGTGGTGGAGGGTG 358
QY 368 GAGGTGGCTCTGGCGGTGGCCGATCGGATGATGAGTCAACCAAGTCTCCAGCAATCATGT 427
DB 359 GTGGGGGAGTGGCGCGGCGGCTCTCAAAATTGTTCTCAACCAAGTCTCCAGCAATCATGT 418
QY 428 CTGCATCTCCAGGGGAGAGGATCAACCATGACCTGCAAGTCCAGTTCAAGTGAAGTACA 487
DB 419 CTGCATCTCCAGGGCCAGAGAGTCAACCATGACCTGCAAGTCCAGTCAAGTGAAGTACA 478
QY 488 TGAACCTGTTCCAAACGAAAGTCAAGGACCTCCCGCCAAAAGATGATTTATGACATCCA 547
DB 479 TGCACCTGGTGAACGAGCAAGAGTCAAGGACCTCCCGCCAAAAGATGATTTATGACATCCA 538
QY 548 AACTGCTTCTGAGAGTCCCTGCTGCTTGAAGTGGAGTGGGTCTGGAACTTTACTCTTC 607
DB 539 AACTGCTTCTGAGAGTCCCTGCTGCTTGAAGTGGAGTGGGTCTGGAACTTTACTCTTC 598
QY 608 TCACATTCAGCAGCATGAGAGCTGAAGATGCTGCCACTTACTACTGCCAGAGTGAAGTA 667
DB 599 TCACATTCAGCAGCATGAGAGCTGAAGATGCTGCCACTTACTACTGCCAGAGTGAAGTA 658
QY 668 GTAACCACTCAAGTTCGGTGGTGGGACCAAGCTGAGAGCTGAAGCG 713
DB 659 GTAACCACTCAAGTTCGGTGGTGGGACCAAGCTGAGAGCTGAAGCG 704

RESULT 8
US-08-564-164A-1
; Sequence 1, Application US/08564164A
; Patent No. 6159947
; GENERAL INFORMATION:
; APPLICANT: Schweighofer, Fabien
```

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; APPLICANT: Tocque, Bruno
; TITLE OF INVENTION: Intracellular Binding Proteins and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcoia Road, 3643
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,164A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00714
; FILING DATE: 15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93/07241
; FILING DATE: 16-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin F.
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: ST93030-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3816
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 858 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..858
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 442..486
; OTHER INFORMATION: /product= "Linker"
; NAME/KEY: misc feature
; LOCATION: 82..810
; OTHER INFORMATION: /product= "ScFv anti-Ras"
US-08-564-164A-1

Query Match      48.6%; Score 462.2; DB 3; Length 858;
Best Local Similarity 77.0%; Pred. No. 1e-122;
Matches 598; Conservative 0; Mismatches 158; Indels 21; Gaps 2;

QY 1 ATGGCCGAGGTCAAGCTGACGAGTCAAGGGGAGGCTTAGTGCAGCTGAGAGGTCCCGG 60
DB 76 ATGGCTCAGGTGAACCTGACGACGACGAGAGAGGCTTAGTGCAGCTGAGAGGTCCCTG 135
QY 61 AAACCTCTCTGAGAGCTCTGATTCATTCACTTCACTAGTACCTTTGGAAATGACATGGTTCG 120
DB 136 AAACCTCTCTGATGATCTCTGATTCATTCACTTCACTAGTACCTTTGAATGACATGGATTCGC 195
QY 121 CAGGCTCAGAGAAAGGGGCTGAGTGGTGGCATATATTAGTAGTGGCAGTAGTACCATC 180
DB 196 CAGACTCCAGGGAAGGAGCTGAGTGGGTGCATTCATTAGTAGTGAAGTGAAGTAACTTACCCTC 255
QY 181 TACTATGAGACACAGTGAAGGAGCATTCACCATCTCCAGAGCAATCCCAAGAACACC 240
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Db 256 TACTATGAGAAACGGTGAAGGGCCGATTCACCATCTCCAGAGACAAATGCCAAGAACACC 315  
 Qy 241 CTGTTCTCTGCAATATGACAGAGTCTTAAGTCTGAGAGACAGGCTCATATTACTGTGCAAGA 300  
 Db 316 CTGTACTCTCAATATGACAGTCTGAGAGTCTGAGAGACAGTCTGATTTATCTGTGCAAGA 375  
 Qy 301 GATTACG-----GGCTTATTTGGGGCCAGAGAACCAACGCTCACCGTTC 342  
 Db 376 CATGAGGGGTACGGGTACCGACTTCTTTGATTTACTGGGGCCAGAGAACCAACGCTCACCGTTC 435  
 Qy 343 TCTCTGAGGTGAGAGCGGCTCAGGCGAGAGGTGCTCTGGCGGTGGCGGATTCGACATTGAG 402  
 Db 436 TCTCTGAGGTGAGAGCGGCTCAGGCGAGAGGTGCTCTGGCGGTGGCGGATTCGACATTGAG 495  
 Qy 403 CTCACCCAGTCTCCAGCAATCATGTCTGATCTCCAGGGAGAGGGTTCACATGACCTGC 462  
 Db 496 CTCACCCAGTCTCCAGCAATCATGTCTGATCTCTGGAGAGAACTGTCTTCATGCAATGT 555  
 Qy 463 AGTGCCAGT---TCAAGTGAAGTACATGAACTGGTTCACAGAGAGTCAAGGACCTCC 519  
 Db 556 CTAGCAAGTGAAGGCAATTCATTAATTTAGCGTGGATCAGCAGAGCCAGGGAATCT 615  
 Qy 520 CCGCAAAAGATGATTTATGACATCCAACTGTCTTGGAGTCCCTGCTGCTTCACT 579  
 Db 616 CCTCAGCTCTGATCTTATTAATGCAAGTCTGAGAGTGGGGTCCCATCAAGGTTCACT 675  
 Qy 580 GGCAGTGGGTCTGGAGCTCTTACTCTCTCAATCAGAGCATGAGAGGCTGAAGTGTCT 639  
 Db 676 GGCAGTGGATCTGGACACAGTCTTCTTCAGATCAGCAACTGCAACTGAAATGAA 735  
 Qy 640 GGCACCTTACTTCCAGCAGTGAAGTGAACCACTCACTGCTGGGTGGAGACCAAG 699  
 Db 736 GGGGTTTATTAATGCTCAACAGGCTTCAAGATCTTCCAGCGTTGAGCTGGACCAAG 795  
 Qy 700 CTGAGACTGAAGCGGCGCGCGGCAAGAACTCATCTCAGAAAGATCTGAT 756  
 Db 796 CTGGAATAAAGCGGCGCGCGGCAAGAACTCATCTCAGAAAGATCTGAT 852

## RESULT 9

US-09-674-677-4  
 ; Sequence 4, Application US/09674677  
 ; Patent No. 6562622  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cola, et al.  
 ; TITLE OF INVENTION: CONTINUOUS IN-VITRO EVOLUTION  
 ; FILE REFERENCE: 674537-2003  
 ; CURRENT APPLICATION NUMBER: US/09/674, 677  
 ; CURRENT FILING DATE: 2000-12-11  
 ; PRIOR APPLICATION NUMBER: PCT/AU99/00341  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: AU PP3445  
 ; PRIOR FILING DATE: 1998-05-08  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 807  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (1)-(807)  
 ; OTHER INFORMATION: Sequence of the anti-hepatitis surface antigen (4c2) scfv  
 ; Patent No. 6562622  
 US-09-674-677-4

Query Match 48.4%; Score 460.2; DB 4; Length 807;  
 Best Local Similarity 77.5%; Pred. No. 3, 7e-122;  
 Matches 574; Conservative 0; Mismatches 158; Indels 9; Gaps 1;  
 Qy 1 ATGGCCGAGTCAAGTGCAGAGTCAAGGGGAGGCTTAACTGACGCTGAGGGCTCCCG 60  
 Db 3 ATGGCCGAGTCAAGTGCAGAGTCAAGGGGAGGCTTAACTGACGCTGAGGGCTCCCG 62

Qy 61 AAATCTCTGTCAGACCTCTGATTCACCTTACAGTACGTTGGAATGCACTGGGTTCTG 120  
 Db 63 AGATTACCTGCAAGGGTTCCGGCTACATTCATCATGATTATGCTATGATGGGGAAG 122  
 Qy 121 CAGGCTCCAGAGAGGGGCTGAGTGGTTCGATATTTATTTAGTGGCAATGATACATC 180  
 Db 123 CAGAGTCATGCCAAGAGTCTAGAGTGAATTTGACCTTATTAATTCCTTTGGTATACA 182  
 Qy 181 TACTATGACAGACAGTGAAGGAGATTCACCATCTCCAGAGCAATCCCAAGAACACC 240  
 Db 183 AACTACACCGAGAGTTTGAAGCCAGGCCACATATCTGTAGACAAATCTTCAACACA 242  
 Qy 241 CTGTTCTCTGCAATATGACAGTCTTAAGTCTGAGAGACCGTCAATGATTAATCTGCAAGA 300  
 Db 243 GGCTATTGGAATCTTGAGATTTGATCATGTGAGGATTTGCGCATTTATTAATGTCAGAA 302  
 Qy 301 G-----ATTACGGGCTTATTTGGGCAAGGACCAACGCTCACCGTCTCTCAAGT 351  
 Db 303 GTGATGACCTGGTCTTTCATGTCTGGGGCCAAAGGACCAACGCTCACCGTCTCTCAAGT 362  
 Qy 352 GAGAGCGGCTCAGGCGGAGGTGCTGGCGGTGGAGATCGGACATTTAGCTCACCCAG 411  
 Db 363 GAGGCGGTTCAAGCGGAGGTGCTGGCGGTGGAGATCGGACATTTAGCTCACCCAG 422  
 Qy 412 TCTCCAGCATCATGTCTGATCTCCAGGGGAGAGGGTCAACATGACCTGAGTGCAGT 471  
 Db 423 TCTCCAGCATCATGTCTGATCTCCAGGGGAGAGGGTCAACATGACCTGAGTGCAGT 482  
 Qy 472 TCAAGTGAAGTACATGAATCTGTTCCACAGAGTCAAGGACCTTCCCAAGAGTGG 531  
 Db 483 TCAAGTGAAGTACATGAATCTGTTCCACAGAGTCAAGGACCTTCCCAAGAGTGG 542  
 Qy 532 ATTATGACATCCAACTGCTTCTGAGTCCCTGCTGCTTCACTGAGTGGAGTGTCT 591  
 Db 543 ATTATGACATCCAACTGCTTCTGAGTCCCTGCTGCTTCACTGAGTGGAGTGTCT 602  
 Qy 592 GGGACCTTACTCTCTCAATCAGACAGCATGAGAGTCTGAGTGCATCTCACTAC 651  
 Db 603 GGGACCTTACTCTCTCAATCAGACAGCATGAGAGTCTGAGTGCATCTCACTAC 662  
 Qy 652 TGCAGCAGTGAAGTGAACCACTGACGTTGGTGTGGAGCAAGCTGAGAGTGA 711  
 Db 663 TGCAGCAGTGAAGTGAACCTTCCAGTGGTGTGGAGCAAGCTGAGAGTGA 722  
 Qy 712 CGGGCGGCGCGCAAGCAAAA 732  
 Db 723 CGGGCGGCGCGCAAGTATAA 743

## RESULT 10

US-08-661-052-15  
 ; Sequence 15, Application US/08661052  
 ; Patent No. 5837243  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yashwant M. Deo  
 ; APPLICANT: Joel Goldstein  
 ; APPLICANT: Robert Graziano  
 ; APPLICANT: Chезian Somasundaram  
 ; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD  
 ; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHYE & COCKFIELD  
 ; STREET: 60 State Street, Suite 510  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109-1875  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,052  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/484,172  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1679 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 11..1667  
US-08-661-052-15

Query Match 47.3%; Score 449.6; DB 2; Length 1679;  
Best Local Similarity 73.5%; Pred. No. 5.9e-119;  
Matches 613; Conservative 0; Mismatches 194; Indels 27; Gaps 2;

QY 6 CGAGGTCAAGCTGCGAGGAGCTGAGGGGAGGCTTAGTGCAGCGTCCCGGAACT 65  
DB 838 CGATATCAAACTGCGAGGAGCTGCGGCGAAGCTTGAGGTGAGGAGCCTCAGTCAAGTT 897  
QY 66 CTCCTGTGAGGCTCTGATTCATTTCAGTAGCTTTGGAATGACCTGGGCTTCGTACGCG 125  
DB 898 GTCCGACAGCTTCTGGCTTCAACATTAAAGACTCCTATGACACTGGTTAGGACGAGG 957  
QY 126 TCCAGAGAAAGGCGCTGAGAGTGGGTGCGATATATAGTATGSCAGTAGTACCATCTACTA 185  
DB 958 GCCTGAACAGGGCGCTGAGTGGATGGATGATGATCTCTGAGAAATGGTATGTAAGAATA 1017  
QY 186 TGCACACACAGTGAAGGAGCGATTCACCATCTCCAGAGCAATCCCAAGAAACCCCTGT 245  
DB 1018 TGCCTCCGAGGCTTCAGGGGAGGCGCATTTTATCTACAGACATCTCCAAACAGCCTTA 1077  
QY 246 CCTGCAAAATGACCACTTAAGGCTGAGGAGCAGCGGTATGATTAATG----- 293  
DB 1078 CCTGACGCTGACAGCAGCTGACATCTGAGGACACTGCGCTCTATTTATGTAATGAGGGAC 1137  
QY 294 -----TGCAGAGATTACGGGGCTTATTGGGGCCAAAGGACCAACCGTCTCTCTC 347  
DB 1138 TCCGACTGGGCGGTACTTATGACTACTGGGGCCCAAGGAGCAACGCTCAGCTCTCTC 1197  
QY 348 AGGTGAGGCGGCTGAGGCGGAGGTGGCTCTGGCGGTGGCGGATGGAGATGAGCTAC 407  
DB 1198 AGGTGAGGCGGCTGAGGCGGAGGTGGCTCTGGCGGTGGCGGATGAGAAATGCTCAC 1257  
QY 408 CCAAGTCTCAGCAATCATGCTGCACTTCAGGGGAGAGGGTCAACATGACCTGCAAGTGC 467  
DB 1258 CCAAGTCTCAGCAATCATGCTGCACTTCAGGGGAGAGGGTCAACATGACCTGCAAGTGC 1317  
QY 468 CAGTTCAAGTGAAGGTACATGAACCTGTTCCAAACAGAAAGTACAGGACCTCCCAAAAG 527  
DB 1318 CAGCTCAAGTGAAGGTACATGAACCTGTTCCAGAGCAAGGACCACTTCCCAAACT 1377  
QY 538 ATGATTTATGACACATCCAACTGCTTCTGAGGCTCCGCTGCTTCAAGTGGAGTGG 587  
DB 1378 CTGGATTTATGACACATCCAACTGCTTCTGAGGCTCCGCTGCTTCAAGTGGAGTGG 1437  
QY 588 GTCTGGGAGCTCTTACTCTCTCAATCAGAGACATGAGGCTGGAAGATGTCGCCACTTA 647  
DB 1438 ATCTGGGAGCTCTTACTCTCTCAATCAGAGACATGAGGCTGGAAGATGTCGCCACTTA 1497

QY 648 CTACTGCCAGAGTGGAGTGAATCAACCTACGTTGCGTGTGGAGCCAAAGCTGAGCT 707  
DB 1498 TTACTGCGAGCAACGAGTAGTATCCACTCAGCTTCGTTGCTGGACCAAGCTGAGCT 1557  
QY 708 GAAAGGGCGGCGCGAGAAACAAAACTCATCTCAGAAAGATCTGAAATGGGGCGGTGCA 767  
DB 1558 GAAAGGGCGGCG-----AGCTGAGCGAGGCGGGGGTACCGATATCGCGGCGC 1608  
QY 768 CGAACAAAACACTATCTCAGAAAGATCTGAATGCTGGGCGAGACAGCA 821  
DB 1609 AGAACAAAACACTATCTCAGAAAGATCTGAATGCGCGCGCGCATCAACATCA 1662

RESULT 11  
US-09-188-082-15  
Sequence 15, Application US/09188082  
Patent No. 6270765

## GENERAL INFORMATION:

APPLICANT: Yashwant M. Deo  
APPLICANT: Joel Goldstein  
APPLICANT: Robert Graziano  
APPLICANT: Chezian Somasundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISD  
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,082  
FILING DATE:

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/661,052  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1679 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:

NAME/KEY: CDS  
LOCATION: 11..1667  
US-09-188-082-15

Query Match 47.3%; Score 449.6; DB 3; Length 1679;  
Best Local Similarity 73.5%; Pred. No. 5.9e-119;  
Matches 613; Conservative 0; Mismatches 194; Indels 27; Gaps 2;

QY 6 CGAGGTCAAGCTGCGAGGAGCTGAGGGGAGGCTTAGTGCAGCGTCCCGGAACT 65  
DB 838 CGATATCAAACTGCGAGGAGCTGCGGCGAAGCTTGAGGTGAGGAGCCTCAGTCAAGTT 897  
QY 66 CTCCTGTGAGGCTCTTACTCTCTCAATCAGAGACATGAGGCTGGAAGATGTCGCCACTTA 125

Db	898	GTCTCGACAGCTTCTGGCTTCAACATTAAAGACTCTTAATGCACTGTTGAGGACGGG	957
Qy	126	TCGAGAGAAAGGGCTGAGTGGGTGCATATATTAGTATGTTGGCAGTAGTACCACTCTACTA	185
Db	958	GCCCTGAACAGGGCCTGAGTGGATTGGATTTGATGATCTTAAGATGGTGTACTGTGATA	1017
Qy	186	TGCAGACACAGTGAAGGAGCATTTACCATCTCCAGAGACAATCCCAAGAACACCCGTGT	245
Db	1018	TGCCCCGAAGTTCAGGGCGAAGGCCATTTTACTACAGACATCTCTCCACACAGCCTA	1077
Qy	246	CCTGCAAAATGACCAAGCTTAAGTCTGAGAGACAGGTCACTGATTACTG-----	293
Db	1078	CCTGCAAGTGAAGAGCTGACATCTGAGAGACATGCGCGTCTATTATTATGATGAGGGAC	1137
Qy	294	-----TGCAGAGATTACGGGCTTATTGGGGCCAGAGACCAACGGTCAACCGTCTCTC	347
Db	1138	TCCGACTGGGCGCTACTATTGACTACTGGGGCCAGAGGACCAACGGTCAACCGTCTCTC	1197
Qy	348	AGGTGAGAGGGGCTCAGGCGGAGGTGGCTGGGGGTGGGGGATTCGACATTGAGCTCAC	407
Db	1198	AGGTGAGAGGGGTTTCAGGCGGAGGTGGCTGGGGGTGGGGGATTCAGAAAATGTGCTAC	1257
Qy	408	CCAGTCTTCAGCAATCAATGTCGTGATCTCCAGGGAGAGGGTTCACATGACCTGCAAGTC	467
Db	1258	CCAGTCTTCAGCAATCAATGTCGTGATCTCCAGGGAGAGGGTTCACATGACCTGCAAGTC	1317
Qy	468	CAGTTCAGTGTAAAGTACATGAACGTGGTCCAACAGAAATCAGGCACTTCCCCCAAAAG	527
Db	1318	CAGCTCAAGTGTAAAGTACATGACACTGGTTCACACAGAAAGCAAGCACTTCTCCAAACT	1377
Qy	528	ATGGAATTATGACACATCCCAACGTCTTCTGAGAGTCCCTGCTGGCTCACTGGCAAGTG	587
Db	1378	CTGGAATTATGACACATCCCAACGTGGCTTCTGAGAGTCCCTGCTGGCTCACTGGCAAGTG	1437
Qy	588	GTCGTGAGACCTTACTCTCTCACAATCAGCAGATGAGGCTGAAGTGTGCACTTA	647
Db	1438	ATCTGGGACCTCTTACTCTCTCACAATCAGCAGATGAGGCTGAAGTGTGCACTTA	1497
Qy	648	CTACTGCCAGACGTGAGTAGTAACCACTACGTTCCGTCTGAGACCAAGCTGAGACT	707
Db	1498	TTACTGCCAGACGTGAGTAGTAACCACTACGTTCCGTCTGAGACCAAGCTGAGACT	1557
Qy	708	GAAACGGGCGGCGGAGAACAAAACTATCTCAGAAAGATCTGAATGGGGCCGTGGA	767
Db	1558	GAAACGGGCGGCGGAGAACAAAACTATCTCAGAAAGATCTGAATGGGGCCGTGGA	1608
Qy	768	CGAACAAAATCTCAATCTCAGAAAGATCTGAATGGTGGGCCAGACAGCA	821
Db	1609	AGAACAAAATCTCAATCTCAGAAAGATCTGAATGGTGGGCCAGACATCACTCA	1662

RESULT 12  
 US-09-364-088-15  
 Sequence 15. Application US/09364088  
 Patent No. 6365161  
 GENERAL INFORMATION:  
 APPLICANT: Yashwant M. Deo, et al.  
 TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISING  
 TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 28 State Street, 24th Floor  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:

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: APPLICATION NUMBER: US/09/364,088
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/188,082
: FILING DATE: 07-JUNE-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/484,172
: FILING DATE: 07-JUNE-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Remillard, Jane E.
: REGISTRATION NUMBER: 38,872
: REFERENCE/DOCKET NUMBER: KRI-043CP2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617)227-7400
: TELEFAX: (617)742-7414
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1679 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 11..1667
:
US-09-364-088-15

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	Query Match .. 47.3%; Score 449.6; DB 3; Length 1679;	
	Best Local Similarity 73.5%; Pred. No. 5,9e-119;	
	Matches 613; Conservative 0; Mismatches 194; Indels 27; Gaps 2	
QY	6 CGAGGTCAAGCTGACGAGAGTTCAGGGGGAGGCTTATGTGACGCTTGAGGGGTCGCCAAACT	65
Db	838 CGATATCAAACTGCAGCAGTCTGGGGGCAAACTGTGAGGTCAAGGACCTCAGTCAAACTT	897
QY	66 CTCTGTGCAAGCCCTGGAATTCATTTTCAGTACGTTTGGATGTGACCTGGGTTCCGACGC	125
Db	898 GTCTTGACAGCTTCTGCTTCAACATTAAAGCTCCATATATGACCTGTTGAGGCAGG	957
QY	126 TCCAGAAAGGGGCTGAGTGGGTTCGCAATATTTAGTAGTGGCAGTAGTACCATTTACTA	185
Db	958 GCCGTGAACAGGGCTCGAGTGGATTGGATGGATTGATCTCTAGATAGTGTGATATCGAATA	101
QY	186 TGCAGACACAGTGAAGGAGCGATTCAACATCTCAGAGACAAATCCCAAGAACCCCTGTT	245
Db	1018 TGCCCGAAGTTCAGGGCAAGGCCACTTTTACTACAGACATCTCTCAACAGCCTA	107
QY	246 CTTGCAATATGACCACTTAAGTCTTGAGAACACGGTCAATGTATTACTG-----	293
Db	1078 CTTGCACCTGACGACCTGACATCTGAGGACACACGCGCTTATTTATTTGATGAGGGGAC	113
QY	294 -----TGCAAGATTTACGGGGCTTTATTTGGGGGCCAAGGAGCAACGGTCAACGTTCTC	347
Db	1138 TCCGACTGGGCGGTACTACTTTTACTCTGAGGGCCAGAGGACCAAGGTCAACGTTCTC	119
QY	348 AGGTGAGGGCGCTCAGGCGGAGGTGCTCTGCGGTGGCGGATCCGACATTGAGCTCAC	407
Db	1198 AGGTGAGGGCGGTTCAAGCGGAGGTGCTCTGCGGTGGCGGATCCAGAAATGTCTCAC	125
QY	408 CCAGTCTTCAGCAATCATGTTTGCAATCTTCCAGGGGAGAGGCTCACATGACTGTGAGTGC	467
Db	1258 CCACTCTCCAGCAATCATGTTTGCAATCTTCCAGGGGAGAGAGGTCAACATTAACCTGCAATGC	131
QY	468 CAGTTCAAGTGAAGTATCATGAATCGGTTCCACAGAAATCAGGCACTCCCCCAAG	527
Db	1318 CAGCTCAAGTGAAGTATCATGCACTGGTTTCCAGCAAGACCAAGCACTTCTCCAACT	137
QY	528 ATGGAATTTATGACATCCAAACTGTTCTTGAGATCCCTGCTCGCTTCAATGCGCAGTGG	587
Db	1378 CTGGAATTTATGACATCCAACTGGCTTCTGAGATCCCTGCTCGCTTCAATGCGCAGTGG	143
QY	588 GTCTGGGACCTTACTCTCTCAAAATTCAGACGATGAGGCTGAAGTGTCTGCCACTTA	647

Db 1438 ATCTGGAGCTCTTACTCTCTCAATCAGCCGAATGAGGCGTGAAGATGCTGCCACTTA 1497  
Qy 648 CTACTGCCAGCTGAGTGAATACCACTCACTGTTGGTGTGGAGCAAGCTGAGCT 707  
Db 1498 TTACTGCGCAGCAACGAGTGAATACCACTCACTGTTGGTGTGGAGCAAGCTGAGCT 1557  
Qy 708 GAAACGGGCGCGCGAGAACAAAATCTCATCTCAGAAAGAGATCTGAATGGGGCGGTGCA 767  
Db 1558 GAAACGGGCGCGC-----AGGCTCGAGCGAGCGGGGGAGGAGATATGCGCGCGC 1608  
Qy 768 CGAACAAAATCTCATCTCAGAAAGAGATCTGAATGCTGTGGCGCAGACCGCA 821  
Db 1609 AGAACAAAATCTCATCTCAGAAAGAGATCTGAATGGCGCGCAGCATCACTCA 1662

## RESULT 13

US-09-102-716-15  
Sequence 15, Application US/09102716  
Patent No. 6395272  
GENERAL INFORMATION:  
APPLICANT: Yashwant M. Deo  
Joel Goldstein  
Robert Graziano  
Chezian Somaundaram  
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED  
OF ANTI-FC RECEPTOR ANTIBODIES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/102,716  
FILING DATE: 22-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/661,052  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MXI-043CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1679 base pairs  
TYPE: nucleic acid  
STRADEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 11..1667  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-102-716-15

Query Match 47.3%; Score 449.6; DB 3; Length 1679;  
Best Local Similarity 73.5%; Pred. No. 5,9e-119;  
Matches 613; Conservative 0; Mismatches 194; Indels 27; Gaps 2;

Qy 6 CGAGGTCAAGCTGCAAGAGTCAAGGCGAGGCTTAACTGACGCTGAGAGGCTCCGGAAACT 65  
Db 838 CGATATCAAACTGACAGAGTCTGGGCGAGAACTTGAGAGTCAAGGAGACTCAAGT 897

Qy 66 CTCTGTGACAGCTCTGATTCATTCACTTACAGTAGCTTTGGAATGCACTGGGTTCGTAGGC 125  
Db 898 GTCTGCAACAGCTTCTGCTTCTTCACTTAAAGCTCTTATATGACCTGGTTGAGCGAGG 957  
Qy 126 TCCAGAGAAAGGGGCTGAGTGGTTCGATATATTAATTAATTAATTAATTAATTAATTA 185  
Db 958 GCTTGAACAGAGGCGCTGAGTGGATTTGATGATGATTTGATGATGATTTGATGATGATTA 1017  
Qy 186 TGCAGACACAGTGAAGGAGCAGATTCACTCCAGAGACAAATCCCAAGAACACCTGTT 245  
Db 1018 TCCCCGAGGATTCAGGGCAGAGCCACTTTTACTACACACATCTCCCAACAGAGCTTA 1077  
Qy 246 CCTGCAATGACCAAGTCTAAGTCTGAGACACAGGTCATATTAATTAATTAATTAATTA 293  
Db 1078 CTTGAGCTGAGACAGCTGACATCTGAGAGACATGCGCTTATTAATTAATTAATTAATTA 1137  
Qy 294 -----TGCAGAGATTAACGGGGCTTATTTGGGGCCCAAGGACCAAGCTCACCTCTCTC 347  
Db 1138 TCCGACTGGGCGATTACTTTGACTACTGGGGCCCAAGGACCAAGCTCACCTCTCTC 1197  
Qy 348 AGGTGAGGCGGCTCAGCGGAGAGTGGCTCTGGCGGTGGCGGATCGACATTAAGCTCAC 407  
Db 1198 AGGTGAGGCGGCTCAGCGGAGAGTGGCTCTGGCGGTGGCGGATCGACAAATGCTCTCAC 1257  
Qy 408 CCAAGTCCAGCAATCATGCTGCATCTCCAGGGGAGAGGTCACATGACCTGAGAGTC 467  
Db 1258 CCAAGTCCAGCAATCATGCTGCATCTCCAGGGGAGAGGTCACATGACCTGAGAGTC 1317  
Qy 468 CAGTTCAGTGAAGTACATGAATGAGTTCACAGAGAGTCAAGACCTCCCAAGAG 527  
Db 1318 CAGTTCAGTGAAGTACATGAATGAGTTCACAGAGAGTCAAGACCTCCCAAGAG 1377  
Qy 528 ATGATTTATGACATATCAAACTGTCTTCTGAGTCCCTGCTGCTTCAAGTGGAGTGG 587  
Db 1378 CTGATTTATGACATATCAAACTGTCTTCTGAGTCCCTGCTGCTTCAAGTGGAGTGG 1437  
Qy 588 GTCTGGGAGCTCTTACTCTCTCAATCAGACAGATGAGGCTGAATGCTGCCACTTA 647  
Db 1438 ATCTGGAGCTCTTACTCTCTCAATCAGACCGAATGAGGCTGAATGCTGCCACTTA 1497  
Qy 648 CTACTGCCAGAGTGAATGAATCCCACTCACTGTTCCGTGTGGAGCAAGCTGAGCT 707  
Db 1498 TTACTGCGCAGCAACGAGTGAATACCACTCACTGTTCCGTGTGGAGCAAGCTGAGCT 1557  
Qy 708 GAAACGGGCGCGCGAGAACAAAATCTCATCTCAGAAAGAGATCTGAATGGGGCGGTGCA 767  
Db 1558 GAAACGGGCGCGC-----AGGCTCGAGCGAGCGGGGGTACGATATCGCGCGCGC 1608  
Qy 768 CGAACAAAATCTCATCTCAGAAAGAGATCTGAATGCTGTGGCGCAGACCGCA 821  
Db 1609 AGAACAAAATCTCATCTCAGAAAGAGATCTGAATGGCGCGCAGCATCACTCA 1662

## RESULT 14

US-09-142-974B-3  
Sequence 3, Application US/09142974B  
Patent No. 645195  
GENERAL INFORMATION:  
APPLICANT: Cheung, Nai-Kong V.  
APPLICANT: Larson, Steven M.  
APPLICANT: Guo, Hong-Fen  
APPLICANT: Rivlin, Ken  
APPLICANT: Sadelain, Michel  
TITLE OF INVENTION: Single chain Fv Constructs of Anti-Ganglioside GD2  
FILE REFERENCE: MSK.P-013-USNP  
CURRENT APPLICATION NUMBER: US/09/142,974B  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: PCT/US97/04427  
PRIOR FILING DATE: 1997-03-20  
PRIOR APPLICATION NUMBER: 60/013,703  
PRIOR FILING DATE: 1996-03-20  
NUMBER OF SEQ ID NOS: 5



SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 1176  
 TYPE: DNA  
 ORGANISM: Murine  
 FEATURE:  
 OTHER INFORMATION: 5F11-scfv-streptavidin  
 NAME/KEY: unsure  
 LOCATION: (37)  
 NAME/KEY: unsure  
 LOCATION: (79)  
 US-09-142-974B-3

Query Match 46.6%; Score 443.6; DB 3; Length 1176;  
 Best Local Similarity 76.6%; Pred. No. 2,6e-117;  
 Matches 558; Conservative 0; Mismatches 161; Indels 9; Gaps 1;

```

QY 8 AGGTCAAGCTGCAGAGAGTCAAGGAGGCTTAACTGACGCTGGAGGGTCCGGAACTCT 67
DB 2 AGGTCAAACTGCAGAGAGTCAAGGAGGCTTAACTGACGCTGGAGGGTCCGGAACTAT 61
QY 68 CCTGTCAGACCTCTGGATTCACTTTCAGTAGAGCTTTGGAATGACCTGGGTTCTCAGGCTC 127
DB 62 CCTGCAAGACTTCTGGAAACAAATTACTGAATACACCATGCACTGGGTGAAGCAGAGACC 121
QY 128 CAGAGAAAGGAGCTGAGAGGCTGAGTATATTAATTAAGTGGCAGTAGTACCATCTACTATG 187
DB 122 ATGGAAGAGGCTGAGAGGCTGAGTATATTAATTAAGTGGTGGTGAATCACTACA 181
QY 188 CAGACACAGTGAAGGAGCATTACCATCTCCAGAGCAATCCCAAGAACCCCTGTTCC 247
DB 182 ACAGAAAGTTCAAGGAGCAGGCAATGACTGTAACAAGTCTCCAGACAGCCTACA 241
QY 248 TGCATAATGACAGCTTAAGTCTGAGAGACCGCTCATATTAATTAATTAAGTGAAGATTACG 307
DB 242 TGAAGCTCCGAGGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 301
QY 308 GG-----GCTTATGGGGCCAGAGGACAGGCTCCTGCTCCTCAGGTGAGGCG 358
DB 302 CGGTCCCTGTTGCTTACTGGGTCCAGAGGACAGGCTCCTCCTCAGGTGAGGCG 361
QY 359 GCTCAGGCGAGGTGCTCTGCGGTGGCGGATCGGACATTGAGCTCACCCAGTCTCCAG 418
DB 362 GTTCAAGCGAGGTGCTCTGCGGTGGCGGATCGGACATTGAGCTCACCCAGTCTCCAG 421
QY 419 CAATCATGCTGATCTCCAGGGGAGAGGCTCACTGACCTGCACTGAGTCCAGTTCAAGTG 478
DB 422 CAATCATGCTGATCTCCAGGGGAGAGGCTCACTGACCTGCACTGAGTCCAGTTCAAGTG 481
QY 479 TAAGTACATGAAGCTGTTCCAGAGAGTCAAGGACCTCCCAAGAAAGATGATTTATG 538
DB 482 TAAGTACATGAAGCTGTTCCAGAGAGTCAAGGACCTCCCAAGAAAGATGATTTATG 541
QY 539 ACACATCAAACTGCTTCTGAGAGTCCCTGCTGCTTCACTGAGTGGAGTGGTCTGGAGCT 598
DB 542 ACACATCAAACTGCTTCTGAGAGTCCCTGCTGCTTCACTGAGTGGAGTGGTCTGGAGCT 601
QY 599 CTATCTCTCTCAAACTGAGAGAGTGAAGTCTGCACTTACTTACTGCGCAGC 658
DB 602 CTATCTCTCTCAAACTGAGAGAGTGAAGTCTGCACTTACTTACTGCGCAGC 661
QY 659 AGTGAAGTGAATCAACCACTCAGGTCGGGCTGGGAGCAAGCTGAGAGTGAAGCGGCGG 718
DB 662 AGTGAAGTGAATCAACCACTCAGGTCGGGCTGGGAGCAAGTGAAGTGAAGCGGCGG 721
QY 719 CCGCAGAA 726
DB 722 CCGCTGGA 729

```

RESULT 15  
 US-09-473-653-5  
 Sequence 5, Application US/09473653

Patent No. 6703015  
 GENERAL INFORMATION:  
 APPLICANT: Solomon, Beka  
 APPLICANT: Frenkel, Dan  
 TITLE OF INVENTION: IMMUNIZATION AGAINST AMYLOID PLAQUES USING DISPLAY TECHNOLOGY  
 FILE REFERENCE: 00/20785  
 CURRENT APPLICATION NUMBER: US/09/473,653  
 PRIOR FILING DATE: 1999-12-29  
 PRIOR APPLICATION NUMBER: 60/152,417  
 NUMBER OF SEQ ID NOS: 24  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 5  
 LENGTH: 717  
 TYPE: DNA  
 ORGANISM: Artificial sequence  
 FEATURE:  
 NAME/KEY: misc.feature  
 LOCATION: (1..1)  
 OTHER INFORMATION: scfv 508f construct  
 US-09-473-653-5

Query Match 46.5%; Score 442; DB 4; Length 717;  
 Best Local Similarity 77.4%; Pred. No. 6e-117;  
 Matches 554; Conservative 0; Mismatches 150; Indels 12; Gaps 1;

```

QY 8 AGGTCAAGCTGCAGAGAGTCAAGGAGGCTTAACTGACAGCCTGGAGGGTCCGGAACTCT 67
DB 2 AGGTCAAACTGCAGAGAGTCAAGGAGGCTTAACTGACAGCCTGGAGGGTCCGGAACTAT 61
QY 68 CCTGTCAGACCTCTGGATTCACTTTCAGTAGAGCTTTGGAATGACCTGGGTTCTCAGGCTC 127
DB 62 CCTGCAAGGCTTCTGGCTACATTCATGATTAATCTATGCTGAGTGGTGAAGCAGAGTCT 121
QY 128 CAGAGAAAGGAGCTGAGAGGCTGAGTATATTAATTAAGTGGCAGTAGTACCATCTACTATG 187
DB 122 ATGGAAGAGGCTGAGAGGCTGAGTATATTAATTAAGTGGTGGTGAATCACTACA 181
QY 188 CAGACACAGTGAAGGAGCATTACCATCTCCAGAGCAATCCCAAGAACCCCTGTTCC 247
DB 182 ACAGAAAGTTCAAGGAGCAGGCAATGACTGTAACAAGTCTCCAGACAGCCTACA 241
QY 248 TGCATAATGACAGCTTAAGTCTGAGAGACCGCTCATATTAATTAATTAAGTGAAGATTACG 307
DB 242 TGAAGCTCCGAGGCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAGAGTCTGAG 301
QY 308 GG-----ATTAAGGAGCTTATTTGGGGCCAGAGGACAGGCTCCTCCTCAGGTGAGG 355
DB 302 CTATGCTCTTAATTTGCTACTGGGGCCAGAGTCAAGGCTCCTCCTCAGGTGAGG 361
QY 356 GCGGCTCAGGCGAGGTGCTCTGCGGTGGCGGATCGGACATTGAGCTCACCCAGTCTC 415
DB 362 GCGGCTCAGGCGAGGTGCTCTGCGGTGGCGGATCGGACATTGAGCTCACCCAGTCTC 421
QY 416 CAGCAATCAATGCTGATCTCCAGGGGAGAGGCTCACTGACCTGCACTGAGTCCAGTTCAA 475
DB 422 CAGCAATCAATGCTGATCTCCAGGGGAGAGGCTCACTGACCTGCACTGAGTCCAGTTCAA 481
QY 476 GTTAAAGTACATGAAGTGGTTCACAGAGAGTCAAGGACCTTCCCAAGAAAGATGATTT 535
DB 482 GTTAAAGTACATGAAGTGGTTCACAGAGAGTCAAGGACCTTCCCAAGAAAGATGATTT 541
QY 536 ATGACATCAAACTGCTTCTGAGAGTCCCTGCTGCTTCACTGAGTGGAGTGGTCTGGAG 595
DB 542 ATGACATCAAACTGCTTCTGAGAGTCCCTGCTGCTTCACTGAGTGGAGTGGTCTGGAG 601
QY 596 CCTTCTACTCTCAAACTGAGAGAGTGAAGTCTGCACTTACTTACTGCGC 655
DB 602 CCTTCTACTCTCAAACTGAGAGAGTGAAGTCTGCACTTACTTACTGCGC 661
QY 656 AGCAGTGAAGTGAATCAACCACTCAGGTCGGGCTGGGAGCAAGCTGAGTGAAGTGAAG 711
DB 662 ATCAGCGAGTGAATCAACCACTCAGGTCGGGCTGGGAGCAAGCTGAGTGAAGTGAAG 717

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Search completed: June 23, 2005, 10:09:31  
Job time : 204 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2005, 05:50:26 ; Search time 23 Seconds  
(without alignments)  
1321.935 Million cell updates/sec

Title: US-09-403-882a-2

Perfect score: 1622  
Sequence: 1 MAEVKLQESGGGLVPGGSR.....VLTITSLITLIMLWQKPR 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79;.\*  
1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	892.5	55.0	268	2 A56446	Ig heavy chain V r
2	718.5	44.3	249	2 S41374	single chain Fv an
3	626.5	38.6	233	2 UCS322	p53 specific singl
4	555.5	34.2	213	2 S68213	Ig heavy chain (Ma
5	535	33.0	136	1 G1M621	Ig heavy chain pre
6	522.5	32.2	121	2 B34871	Ig heavy chain V r
7	516	31.8	130	1 JL0079	Ig kappa chain pre
8	514	31.7	235	2 S25058	Ig kappa chain - m
9	511	31.5	107	2 A30562	Ig kappa chain V r
10	508	31.3	103	2 S29591	Ig kappa chain V r
11	508	31.3	104	2 B49049	Ig kappa chain V r
12	506	31.2	106	2 PS0071	Ig kappa chain V r
13	506	31.2	107	2 B30562	Ig kappa chain V r
14	501	30.9	107	2 S11118	Ig kappa chain V r
15	498	30.7	107	2 S11119	Ig kappa chain V r
16	498	30.7	107	2 PC4405	Ig kappa chain V r
17	490	30.2	107	2 S11121	Ig kappa chain V r
18	488	30.1	107	2 PT0406	Ig kappa chain V r
19	484.5	29.9	143	2 S23624	Ig heavy chain V r
20	483	29.8	107	2 S11117	Ig kappa chain V r
21	482	29.7	120	2 S12953	Ig kappa chain V r
22	481.5	29.7	108	2 G30560	Ig heavy chain V r
23	480	29.6	94	2 D25913	Ig heavy chain V r
24	479	29.5	100	2 S29590	Ig kappa chain V r
25	479	29.5	107	2 S11112	Ig kappa chain V r
26	478	29.3	108	2 PH1015	Ig heavy chain V r
27	476	29.3	107	2 PD0011	Ig kappa chain V r
28	473	29.2	97	2 PH1084	Ig light chain V r
29	473	29.2	114	2 S46392	Ig heavy chain V r

30	471.5	29.1	123	2 S26794	Ig heavy chain V r
31	471.5	29.1	125	2 S30531	Ig heavy chain V r
32	471	29.0	114	2 S46391	Ig heavy chain V r
33	470	29.0	110	2 PH1014	Ig heavy chain V r
34	470	29.0	114	2 S46390	Ig heavy chain V r
35	469	28.9	107	2 S11113	Ig kappa chain V r
36	468.5	28.9	548	2 S38864	Ig epsilon chain C
37	468	28.9	97	2 S26341	Ig light chain V r
38	467	28.8	106	2 G27887	Ig kappa chain V r
39	466	28.7	140	2 S70442	Ig heavy chain pre
40	463	28.5	106	2 B54378	Ig light chain V r
41	462	28.5	104	2 UC6076	anti-D-dimer monoc
42	461.5	28.5	108	2 S38720	Ig light chain V r
43	461.5	28.5	120	2 S55536	Ig heavy chain V r
44	461	28.4	130	2 S04573	Ig kappa chain pre
45	460.5	28.4	120	2 S66536	Ig light chain V r

#### ALIGNMENTS

##### RESULT 1

A56446 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical

A/Reference number: A56446; PMID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotetramer; immunoglobulin

Query Match 55.0%; Score 892.5; DB 2; Length 268;

Best Local Similarity 65.9%; Pred. No. 1.2e-52;

Matches 176; Conservative 26; Mismatches 52; Indels 13; Gaps 2;

QY	1	MAEVKLQESGGGLVPGGSRKLSCAASGFTSSFGHMYRQAEKGLVAVYISGSSSTI	60
DB	1	MAQVKLQESGAEIVKPGASVKLSCTTSGFNIKQTYHMYVQREQGLEWIGRIAPANGIT	60
QY	61	YVADTVKGRFTISRDNPATFLFQMTSLKSEDTVMYYCA---RDYGVYGGGTYTVSS	116
DB	61	KYDPKQGRATVADTSNTRYVQLSLTSEDPVAVYVYLLTRYENVYGGGTYTVSS	120
QY	117	GGGSGGGGGGGGGSDIELTQSPAIMSASPERVITWTCASSSVRYVMNPFQKSGTSPKR	176
DB	121	GGGSGGGGGGGGGSDIELTQSPAIMSASPERVITWTCASSSVRYVMNPFQKSGTSPKR	180
QY	177	WIYDTKLSLGSVGPVAPFSGSGSTYSYLTISMAEDPATYVCOQWSNPLTFGAGTKLEL	236
DB	181	WVYVTSHPGVPVAPFSGSGSTYSYLTISMAEDPATYVCOQFSSPTFGSGTLEI	240
QY	237	KRA-----AAEQKISEEDLNGA	254
DB	241	KRSAAHHHHRGAABQKISEEDLNGA	267

##### RESULT 2

S41374 single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995

C/Accession: S41374

R/Artsenko, O.; Weiler, E.W.; Muenz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibody

A/Reference number: S41374

A:Accession: S41374  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-249 <ART>  
 A:Cross-references: EMBL:Z29480

Query Match 44.3%; Score 718.5; DB 2; Length 249;  
 Best Local Similarity 57.8%; Pred. No. 4.7e-41;  
 Matches 144; Conservative 31; Mismatches 63; Indels 11; Gaps 3;

QY 3 EYKLOSGGGGLVOPGSGSRKLSCAASGFTSSFCGMHWVROAPEKGLFWAVYISSGSSITYY 62  
 DB 1 QVQLQSGGGLVOPGSGSRKLSCAASGFTSSFCGMHWVROAPEKGLFWAVYISSGSSITYY 60  
 QY 63 ADTVKGRFTISRDNPNKNTLFLQMTSLRSEDTVMYICARD---YGA--YWGQGTITVVS 117  
 DB 61 VPRFQOKATITADTSNTAVYLLSLTSEDTAVYICARDRLTSLGVMGQGSITVVS 120  
 QY 118 GGGSGGGGGSDIELTQSPAIMSASPERVYTMTCASASSV-----RYMMWFOQKSG 171  
 DB 121 GGGSGGGGGSDIELTQSPVAVIPGESVYISCRSKSLYSDGDSYLFWFLQRP 180  
 QY 172 TSPKRWIYDTSKLSGVPAFSGSGTSYSLTISMEADATYTCQOMSSNPLTFGAG 231  
 DB 181 QSFQILLIKMSNLASGVDPDRFSGSGSTFTLRISKEADGVYICMQRREPLTFGAG 240  
 QY 232 TKLELRKAA 240  
 DB 241 TKLELRKAA 249

RESULT 3  
 JC5322  
 p53 specific single-chain antibody Pab421 - human

C:Species: Homo sapiens (man)  
 C:Date: 15-May-1997 #sequence\_revision 15-May-1997 #text\_change 18-Jul-1997  
 C:Accession: JC5322  
 R:Jannot, C.B.; Hynes, N.E.  
 Biochem. Biophys. Res. Commun. 230, 242-246, 1997  
 A:Title: Characterization of acFv-421, a single-chain antibody targeted to p53.  
 A:Reference number: JC5322; MUID:97168950; PMID:9016757  
 A:Accession: JC5322

A:Molecule type: mRNA  
 A:Residues: 1-233 <UAN>  
 A:Experimental source: hybridoma cell  
 A:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 38.6%; Score 626.5; DB 2; Length 233;  
 Best Local Similarity 55.3%; Pred. No. 6.1e-35;  
 Matches 131; Conservative 29; Mismatches 66; Indels 11; Gaps 5;

QY 7 QESGGGLVOPGSGSRKLSCAASGFTSSFCGMHWVROAPEKGLFWAVY--SSGSSITYYAD 64  
 DB 1 QESGALVNSGASVYKLSCTTSGFNINDYMMWYKRRPEGLWIGRIDENGDADMTRES 60  
 QY 65 TVKGRFTISRDNPNKNTLFLQMTSLRSEDTVMYICARDYGA YWGQGTITVVS GGGSGG 124  
 DB 61 GYVA--TMTADTSSNTAVYLLSLTSEDTAVYICNAGMD--YWGQGTITVVS SGGSGG 117  
 QY 125 GGGGGSDIELTQSPAIMSASPERVYTMTCASASSV-----RYMMWFOQKSGTSPKRWIY 179  
 DB 118 ASGGGSDIELTQSPVAVIPGESVYISCRSKSLYSDGDSYLFWFLQRP 177  
 QY 180 DTSKLSGVPAFSGSGTSYSLTISMEADATYTCQOMSSNPLTFGAGTKLEI 236  
 DB 178 LVSNLSSGVPAFSGSGSTFTLRISKEADGVYICMQRREPLTFGAG-GRKLEI 233

RESULT 4  
 S68213  
 Ig heavy chain (Mab03-1) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 29-Jul-1997 #sequence\_revision 17-Sep-1997 #text\_change 09-Jul-2004

C:Accession: S68213  
 R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.  
 FEBS Lett. 375, 273-276, 1995  
 A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin  
 A:Reference number: S68211; MUID:96085223; PMID:7498516  
 A:Accession: S68213  
 A:Status: preliminary; nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-213 <TAK>  
 A:Cross-references: UNIPROT:Q91205; EMBL:D29667  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 34.2%; Score 555.5; DB 2; Length 213;  
 Best Local Similarity 53.9%; Pred. No. 3.1e-30;  
 Matches 124; Conservative 17; Mismatches 50; Indels 39; Gaps 5;

QY 4 VKLQSGGGGLVOPGSGSRKLSCAASGFTSSFCGMHWVROAPEKGLFWAVYISSGSSITYYA 63  
 DB 2 VQLVSGGGGLVOPGSGSRKLSCAASGFTSSFCGMHWVROAPEKGLFWAVYISSGSSITYYA 61  
 QY 64 DTVKGRFTISRDNPNKNTLFLQMTSLRSEDTVMYICARDY---GAYWGQGTITVVS GGGG 120  
 DB 62 DTVKGRFTISRDNPNKNTLFLQMTSLRSEDTAVYICARSWLPEFDYWGQGTITVVS 118  
 QY 121 SGGSGGGGGSDIELTQSPAIMSASPERVYTMTCASASSVRYMMWFOQKSGTSPKRWIYD 180  
 DB 119 -----KTPPSVYPLAPGCGDTTGSVTLGLGVGFPESEVTW-----WN 159  
 QY 181 TSKLSSGV---PARFSGSGTSYSLTISMEADATYTCQOMSSNPLT 227  
 DB 160 SGLSSVHTFPALLQSGLYTWSSSVTVPS-----STWPSQTVT 198

RESULT 5

GI521  
 Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
 C:Accession: E90809; A93184; A02066  
 R:Botwell, A.L.M.; Paekhard, M.; Reih, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D.  
 Cell 24, 625-637, 1981  
 A:Title: Heavy chain variable region contribution to the NP(b) family of antibodies: some  
 A:Reference number: A90809; MUID:81234548; PMID:6788376  
 A:Accession: E90809

A:Molecule type: mRNA  
 A:Residues: 1-136 <BOT>  
 A:Cross-references: UNIPROT:P01783; GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055  
 R:Adelung, K.; Milstein, C.; Secher, D.S.  
 Nature 265, 299-304, 1977  
 A:Title: Molecular analysis of spontaneous somatic mutants.  
 A:Reference number: A93184; MUID:77100368; PMID:401950  
 A:Contents: myeloma protein MOPC 21  
 A:Accession: A93184

A:Molecule type: protein  
 A:Residues: 17-74, 'D', 76-77, 'H', 79-88, 'ND', 91-114, 'H', 116-119, 'W', 121-136 <ADE>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterocyclamer; immunoglobulin  
 F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:17-136/Domain: Ig heavy chain V region (MOPC 21) #status experimental <MAT>  
 F:115-119/Region: D segment  
 F:120-136/Region: J segment  
 F:38-112/Disulfide bonds: #status experimental

Query Match 33.0%; Score 535; DB 1; Length 136;  
 Best Local Similarity 87.5%; Pred. No. 4.4e-29;  
 Matches 105; Conservative 5; Mismatches 4; Indels 6; Gaps 2;

QY 3 EYKLOSGGGGLVOPGSGSRKLSCAASGFTSSFCGMHWVROAPEKGLFWAVYISSGSSITYY 62  
 DB 17 DVQLVSGGGGLVOPGSGSRKLSCAASGFTSSFCGMHWVROAPEKGLFWAVYISSGSSITLYH 76





C:/Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
 C:/Accession: S1118  
 R:/Karttunen, M.; Grifflths, G.M.; Markham, A.F.; Milstein, C.  
 Nature 304, 320-324, 1983  
 A:/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone  
 A:/Reference number: S07331; MUID:83271467; PMID:6877353  
 A:/Accession: S1118  
 A:/Status: preliminary  
 A:/Molecule type: mRNA  
 A:/Residues: 1-107 <KAA>  
 C:/Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:/6-89/Domain: immunoglobulin homology <IMM>

Query Match 30.7%; Score 501; DB 2; Length 107;  
 Best Local Similarity 91.5%; Pred. No. 6,4e-27;  
 Matches 97; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 133 IELTQSPALMSAPGERVTMTCSASSSVRYMNFQCKSGTSPKRWIYDTSKLSGVPARF 192  
 |||||  
 DB 2 IYLTQSPALMSAPGERVTMTCSASSSVRYMNFQCKSGTSPKRWIYDTSKLSGVPARF 61  
 |||||

QY 193 SGGSGGTSLTSSMEAPDAITYCCQWSSNPLTFGAGTKLEKR 238  
 |||||  
 DB 62 SGGSGGTSLTSSMEAPDAITYCCQWSSNPLTFGAGTKLEKR 107  
 |||||

## RESULT 15

S1119  
 Ig kappa chain V region (clone NO6-8.3.1) - mouse (fragment)  
 C:/Species: Mus musculus (house mouse)  
 C:/Date: 19-Mar-1997 #sequence\_revision 23-Aug-1997 #text\_change 21-Jan-2000  
 C:/Accession: S1119  
 R:/Karttunen, M.; Grifflths, G.M.; Markham, A.F.; Milstein, C.  
 Nature 304, 320-324, 1983  
 A:/Title: mRNA sequences define an unusually restricted IgG response to 2-phenylloxazalone  
 A:/Reference number: S07331; MUID:83271467; PMID:6877353  
 A:/Accession: S1119  
 A:/Molecule type: mRNA  
 A:/Residues: 1-107 <NAT>  
 C:/Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:/6-89/Domain: immunoglobulin homology <IMM>

Query Match 30.7%; Score 498; DB 2; Length 107;  
 Best Local Similarity 89.6%; Pred. No. 1e-26;  
 Matches 95; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 133 IELTQSPALMSAPGERVTMTCSASSSVRYMNFQCKSGTSPKRWIYDTSKLSGVPARF 192  
 |||||  
 DB 2 IYLTQSPALMSAPGERVTMTCSASSSVRYMNFQCKSGTSPKRWIYDTSKLSGVPARF 61  
 |||||

QY 193 SGGSGGTSLTSSMEAPDAITYCCQWSSNPLTFGAGTKLEKR 238  
 |||||  
 DB 62 SGGSGGTSLTSSMEAPDAITYCCQWSSNPLTFGAGTKLEKR 107  
 |||||

Search completed: June 23, 2005, 05:50:58  
 Job time : 24 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 23, 2005, 05:50:26 ; Search time 83 seconds  
(without alignments)  
1949.603 Million cell updates/sec

Title: US-09-403-882a-2  
Perfect score: 1622  
Sequence: 1 MAEVKLQESGGGLVQPGGSR.....VLLTISLILMLMOKKPR 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	893	55.1	240	2 Q65ZC9	Q65ZC9 homo sapien
2	853.5	52.6	298	2 Q9QYF0	Q9QYF0 synthetic c
3	850	52.4	255	2 Q6KB05	Q6KB05 mus musculu
4	790.5	48.7	248	2 Q65Z07	Q65Z07 mus sp. b3(
5	733	45.2	244	2 Q65ZC8	Q65ZC8 homo sapien
6	707	43.6	247	2 Q65ZL2	Q65ZL2 mus sp. fv/
7	695	42.8	241	2 Q921A6	Q921A6 mus musculu
8	658	40.6	243	2 Q7TQM2	Q7TQM2 mus musculu
9	608.5	37.5	218	2 Q925S1	Q925S1 mus musculu
10	543	33.5	485	2 Q6PDB8	Q6PDB8 mus musculu
11	542	33.4	473	2 Q91Z05	Q91Z05 mus musculu
12	535	33.0	136	1 HV16_MOUSE	Q91703 mus musculu
13	507	31.3	107	1 KV6F_MOUSE	P04940 mus musculu
14	506	31.2	107	1 KV6H_MOUSE	P04942 mus musculu
15	502	30.9	107	1 KV6I_MOUSE	P04943 mus musculu
16	500	30.8	107	1 KV6G_MOUSE	P04941 mus musculu
17	498	30.7	112	2 Q6K1F0	Q6K1F0 mus musculu
18	494	30.5	107	1 KV6J_MOUSE	P04944 mus musculu
19	484.5	29.9	487	2 Q99K44	Q99K44 mus musculu
20	483	29.6	134	2 Q8VDD0	Q8VDD0 mus musculu
21	480	29.6	112	2 Q8K1F2	Q8K1F2 mus musculu
22	473.5	29.2	464	2 Q6MZ06	Q6MZ06 homo sapien
23	473	29.2	472	2 Q6N0B9	Q6N0B9 homo sapien
24	468.5	28.9	473	2 Q6MZV7	Q6MZV7 homo sapien
25	462.5	28.5	113	2 Q9UL90	Q9UL90 homo sapien
26	462	28.5	478	2 Q6P181	Q6P181 homo sapien
27	462	28.4	613	2 Q8WUK1	Q8WUK1 mus musculu
28	461	28.3	112	2 Q8K1F3	Q8K1F3 mus musculu
29	459	28.3	470	2 Q6PJ44	Q6PJ44 homo sapien
30	458	28.2	114	2 Q8K1F1	Q8K1F1 mus musculu
31	454.5	28.0	597	2 Q96BB9	Q96BB9 homo sapien

32	452.5	27.9	119	2 Q920E7	Q920E7 mus musculu
33	450	27.7	606	2 Q6GMV2	Q6GMV2 homo sapien
34	449	27.7	466	2 Q6IN78	Q6IN78 homo sapien
35	446	27.5	107	1 KV6C_MOUSE	P01677 mus musculu
36	445	27.4	118	2 Q9UL51	Q9UL51 homo sapien
37	443	27.3	465	2 Q6PEC4	Q6PEC4 homo sapien
38	443	27.3	479	2 Q91WP5	Q91WP5 mus musculu
39	441	27.2	107	1 KV6B_MOUSE	P01676 mus musculu
40	440.5	27.2	116	2 Q9UL93	Q9UL93 homo sapien
41	440	27.1	107	1 KV6D_MOUSE	P01678 mus musculu
42	439.5	27.1	484	2 Q96K68	Q96K68 homo sapien
43	439	27.0	486	2 Q91Z07	Q91Z07 mus musculu
44	438.5	27.0	131	2 Q811C3	Q811C3 mus musculu
45	438.5	27.0	544	2 Q6PJ95	Q6PJ95 homo sapien

## ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	240 AA.
ID Q65ZC9			
AC Q65ZC9			
DT 25-OCT-2004 (TREMBLrel. 28, Created)			
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE Single-chain Fv (Fragment).			
GN Name=ScFv;			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX NCBI_TaxId=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=C1q/7;			
RA MEDLINE=97362799; PubMed=9219263;			
RX Kontermann R.E., Wing M.G., Winter G.;			
RT "Complement recruitment using bispecific diabodies";			
RL Nat. Biotechnol. 15:629-631(1997).			
DR EMBL: Y13056; CAA73499.1; -.			
DR InterPro: IPR003599; IG.			
DR InterPro: IPR007110; IG_1like.			
DR InterPro: IPR003596; IG_v.			
DR Pfam: PF00047; IG_2.			
DR SMART: SM00409; IG_2.			
DR SMART: SM00406; IGv_2.			
DR PROSITE: PSS0835; IG_1like; 2.			
FT NON_TER 1			
FT NON_TER 240			
FT NON_TER 240			
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;			

Query Match 55.1%; Score 893; DB 2; Length 240;

Best Local Similarity 70.4%; Pred. No. 1.3e-57; Matches 169; Conservative 32; Mismatches 35; Indels 4; Gaps 2;

QY	3	EVLKQESGGGLVQPGGSRKLSCAASGFTFSSFGHWRQAPKGLKLEWVAIYSSGSSITYY	62
DB	1	QVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYGMHWRAQPKGLEWVAIYISYGSNKYY	60
QY	63	ADTVKGRFTISRNPKNVTLFLQMTSLRSEDVTWYICARDYGV--WGQTTVTVSSGGG	119
DB	61	ADSVKGRFTISRDNKNTLYLQNMNLSLAEDTAVYVCARDWGDSLPKGGTLTVVSSGGG	120
QY	120	GSGGGGSGGSGSDIELTQSPALMSASGERVTMTCASSSV--RYMMFQOKSGTSPKRWI	178
DB	121	GSGGGGSGGSGSDIQMTQSPSTLSASISGRVTTTCRASISGITYWLAAYQKPGAPFLTI	180
QY	179	YDTSKLSGVPARFSGSGSTSYSLRTISSWEADDAATYYCQQMSNPLTGAQTKLEIKR	238
DB	181	YKASLSLASRAPRFSGSGSTDTLTITISLQPDPAFYTCQYISNYLTTCGGTKLEIKR	240

RESULT 2

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Q9QYF0 PRELIMINARY; PRT; 298 AA.
ID Q9QYF0;
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CN 8 string chain antibody.
GN Name=CN 8 scfv;
OS synthetic construct.
OC other sequences; artificial sequences.
OX NCBI_Taxid=32630;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;
RA Shiohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA8633.1; -.
DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSSP; P01820; 1A70.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003586; Ig_v.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 52.6%; Score 853.5; DB 2; Length 298;
Best Local Similarity 66.3%; Pred. No. 1.3e-54;
Matches 163; Conservative 32; Mismatches 46; Indels 5; Gaps 2;

QY 1 MAEVKLOESGGGLVQPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLWVAVYISGSSSTI 60
DB 38 MAQVTKLQSGGGGVKXGSLKSCAASGSDPSRMYMSWRQAPGKLEWIGEINPSSSTI 97
QY 61 YYADTVKGFRTISRDNPKNTLFLQMTSLRSEDVWYYCAR---DYGAYWGCGTTTVVS 116
DB 98 NYTPSLKDXPFIISRDNPKNTLYLQMSKXVSEDTALYYCARASYGHSAVWGCGTTTVVS 157
QY 117 GGGSGSGGGSGGGSDIELTQSPAIMSASPGERVMTTCASASSV-RYMMWFOOKSGTSRK 175
DB 158 GGGSGSGGGSGGGSDIELTQSPASISASVGEVTVITCRASGHNYLWYQOKGKSPQ 217
QY 176 RWIYDTSKLSGVPARFSGSGSTSYSLTISMEADATYYCQCMSSNPLTFGAGTKLE 235
DB 218 LLYVNAKTLADGVPSRFSGSGSTQYSLKINSLQPEDPSGYCQHWTTPYFGGGTKLE 277
QY 236 LKRAAA 241
DB 278 IKRAAA 283

RESULT 3
Q6KB05 PRELIMINARY; PRT; 255 AA.
ID Q6KB05;
AC Q6KB05;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Scfv B8E5 protein (Fragment).
GN Name=scfv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hoebeke J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AJ746180; CAG34081.1; -.
DR HSSP; P01837; 1KCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 52.4%; Score 850; DB 2; Length 255;
Best Local Similarity 67.1%; Pred. No. 2e-54;
Matches 167; Conservative 29; Mismatches 39; Indels 14; Gaps 4;

QY 3 EYKLOESGGGLVQPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLWVAVYISGSSSTIY 62
DB 1 QVQLQSGSDLVKPPGSLKVSCAASGFTFSSIGMHVNRQTPDKRLWVAVITISGSSYTY 60
QY 63 ADTVKGFRTISRDNPKNTLFLQMTSLRSEDVWYYCAR--DY--GA--YWGCGTTTVVS 115
DB 61 PDSVKGRTFISRDNPKNTLYLQMSLSKSEDTALYYCARHINRYDGAFDYWGCGTTTVS 120
QY 116 SGGSGSGGGSGGGSDIELTQSPAIMSASPGERVMTTCASASSV-----RYMMWFOO 168
DB 121 SGGSGSGGGSGGGSDIVMAQSPSLVSAAEKVIMSKSQSLNSRNQNYLAWYQO 180
QY 169 KSGTSPKWIYDTSKLSGVPARFSGSGSTSYSLTISMEADATYYCQCMSSNPLTF 228
DB 181 KKGQSPKLLIYASVRESGVPRFTGSGSGDTFTLTISVQMEDLAVYYCQNDHGYPLTF 240
QY 229 GAGTKLEIK 237
DB 241 GAGTKLEIK 249

RESULT 4
Q6SZ07 PRELIMINARY; PRT; 248 AA.
ID Q6SZ07;
AC Q6SZ07;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE B3 (Fv) -PE40 (Fragment).
GN Name=B3 (Fv) -PE40;
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92020904; PubMed=1924323;
RA Brinkmann U., Pal L.H., Fitzgerald D.J., Wittingham M., Pastan I.;
RT "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT regression of a human carcinoma in mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR EMBL; S57990; AAB1971.2; -.
DR InterPro; IPR003589; Ig.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003586; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 248
SQ SEQUENCE 248 AA; 26634 MW; 7A3759B43B570950 CRC64;

Query Match 48.7%; Score 790.5; DB 2; Length 248;
Best Local Similarity 62.6%; Pred. No. 4.4e-50;
Matches 154; Conservative 29; Mismatches 52; Indels 11; Gaps 2;

QY 3 EYKLOESGGGLVQPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLWVAVYISGSSSTIY 62
DB 1 EYKLOESGGGLVQPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLWVAVYISGSSSTIY 62

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Db      2 DVKLVSGGGLVPGGSLKLSKATSGFTSDYMYWVRQTEKRLWVAVISNDSSAAV 61
Qy      63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDPTVMYVYCARD-----YGAYMGQGTTVVSSG 117
Db      62 SDTVKGRFTISRDNPKNTLFLQMTSLRSEDPTVMYVYCARD-----YGAYMGQGTTVVSSG 121
Qy      118 GGGSGGGGGGGGGSDIELTQSPAIMSAPGERVMTCSASSV-----RYNMFPQKSG 171
Db      122 GGGSGGGGGGGGGSDVLTQSPAIMSAPGERVMTCSASSV-----RYNMFPQKSG 181
Qy      172 TSPKMTIYDTSKLSGVPARFSSGSGTSLTISMEADAAATYYCOQMSNPLTFGAG 231
Db      182 QSFKLIYKXSNRFGVPRFSSGSGTDTLKRISRAEDLVGYVCFQSHVPTFGSG 241
Qy      232 TKLEIK 237
Db      242 TKLEIK 247

RESULT 5
065ZC8      PRELIMINARY;      PRT;      244 AA.
AC      065ZC8;
DT      25-OCT-2004 (TREMBLrel. 28, Created)
DT      25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE      25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE      Single-chain Fv (Fragment).
GN      Name=scfv;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97362799; PubMed=9219263;
RA      Kontermann R.E., Wing M.G., Winter G.;
RT      "Complement recruitment using bispecific antibodies.";
RL      Nat. Biotechnol. 15:629-631(1997).
DR      EMBL; Y13057; CAA73500.1; -
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF00047; Ig_2.
DR      SMART; SM00409; Ig_2.
DR      SMART; SM00406; Ig_2.
DR      PROSITE; PS50835; IG_LIKE; 2.
FT      NON_TER      1
FT      NON_TER      244
SQ      SEQUENCE      244 AA; 26127 MW; 4B1F17668338F2BF CRC64;

Query Match      45.2%; Score 733; DB 2; Length 244;
Best Local Similarity 56.6%; Pred. No. 7.2e-46;
Matches 138; Conservative 45; Mismatches 53; Indels 8; Gaps 3;

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RESULT 6
065ZL2      PRELIMINARY;      PRT;      487 AA.
AC      065ZL2;
DT      25-OCT-2004 (TREMBLrel. 28, Created)
DT      25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE      25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE      Fv/M4.
GN      Name=M4-IFN- $\epsilon$ tau>;
OS      Mus sp.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxId=10095;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96272580; PubMed=8688499;
RA      Qi Y., Xiang J.;
RT      "A genetically engineered single-gene-encoded anti-TAG72 chimeric
RT      antibody secreted from myeloma cells.";
RL      Hum. Antibodies Hybridomas 6:161-166(1995).
DR      EMBL; S82493; AAB37424.2; -
DR      InterPro; IPR003599; Ig.
DR      InterPro; IPR007110; Ig-like.
DR      InterPro; IPR003597; Ig_c1.
DR      InterPro; IPR003598; Ig_c2.
DR      InterPro; IPR003006; IG_MHC.
DR      InterPro; IPR003596; Ig_v.
DR      Pfam; PF07654; C1-set; 2.
DR      Pfam; PF00047; Ig_4.
DR      SMART; SM00409; Ig_3.
DR      SMART; SM00407; IGc1; 2.
DR      SMART; SM00408; IGc2; 2.
DR      SMART; SM00406; Ig_2.
DR      PROSITE; PS50835; IG_LIKE; 4.
DR      PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ      SEQUENCE      487 AA; 53578 MW; C7BAB69F30555504 CRC64;

Query Match      43.6%; Score 707; DB 2; Length 487;
Best Local Similarity 54.2%; Pred. No. 1.3e-43;
Matches 129; Conservative 46; Mismatches 59; Indels 4; Gaps 3;

```

RP	SEQUENCE FROM N.A.
RX	MEDLINE=98170165; PubMed=9509426;
RA	Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA	Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT	"Cloning and characterization of cDNAs encoding VH and VL of a
RT	monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT	generation of a single-chain Fv molecule (scFv).";
RL	Mol. Cells 7:816-819(1997).
DR	EMBL; U08067; AAB48044.1; .
DR	PIR; S19965; S19965.
DR	PIR; S19967; S19967.
DR	PIR; S19968; S19968.
DR	PIR; S26325; S26325.
DR	HSSP; P01607; IBMW.
DR	SMART; SMO0406; IGV; 2.
DR	PROSITE; PSS0835; IG_LIKE; 2.
FT	NON_TER
FT	NON_TER
SQ	SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match	42.8%	Score 695	DB 2	Length 241
Best Local Similarity	55.7%	Pred. No.	4,4e-43	
Matches 137	Conservative 40	Mismatches 55	Indels 14	Gaps 5

Qy	3	EVKLQESGGGGLVQPGSGSRKLS	CAASGFFSSFGHMWVQAPEKGL	EWAVIYSSG	STIYY	62
Db	1	QVTLQSGSGPELKKRGETVKIS	CKASGYFTFDYGMNVMWQAAGKGL	KMMGMVINTYTG	DEPTY	60
Qy	63	ADIVYKGRFTISRNDPKNTL	FLQMTSLNSEDTVMY	CAAD---	YGAVYGCGTTVYSSGG	118
Db	61	ADDPKGRFAFLETSAS	FAYLQINNLKNEDATYFC	AKDLRLRF	FDYGGGTTVYVSSGG	120
Qy	119	GGSGGGSGGGSDIELTQSP	PAIMASPEGEVMTWC	SSSV-RYMN	FOOKSGTSPRR-	176
Db	121	GGSGGGSGGGGSDIELTQSP	SSLSASLGGKVTITCK	SPQINKIYANQHK	PGKGPSA	180
Qy	177	---MIYDTSKLSGV	PARFSGSGSGTSYSLTSS	MEADAAITYY	COQSSNPLTF	AGACT 233
Db	181	HTLTIT---	IQPISPRFSGSGSGGRDYS	FSISNLEPED	DIATYCLAH-DNLHTF	GGCTK 235
Qy	234	LELRA	239			
Db	236	LELRA	241			

```

RESULT 8
Q7TOM2
ID Q7TOM2 PRELIMINARY; PRT; 243 AA.
AC Q7TOM2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE ScFv 6H8 protein (Fragment).
GN Name=scFv 6H8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxonomy=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RX MELJINE:22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA Peter J.C., Eftekhari P., Billiard P., Wallukat G., Hoebeke J.;
RT "scFv single chain antibody variable fragment as inverse agonist for
the beta-2 adrenergic receptor."
JT J. Biol. Chem. 278:36740-36747(2003).
DR EMBL; AJ574851; CAE00495.1; -.
DR HSSP; P01751; 1A6W.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV_2.
DR PROSITE; PS50835; IG_LIKE; 2.
NT NON_TER 1 1

```

SQ SEQUENCE 243 AA; 25976 MW; BEEFF64D2DCFAF76 CRC64;

Query Match Similarity	40.6%	Score 658	DB 2	Length 243
Best Local Similarity	53.1%	Pred. No. 2,3e-40		
Matches 127, Conservative	43	Mismatches 65	Indels 6	Gaps 4

**Oy**

3 EVLKQESGGGLVOPGSGRKLSCAASGFTESSIGMHWWRQAPEKGLEWVAIYISSGSITYY 62  
::|::| | ::|| ||||||| :|::| | :|::| |  
**Dd**

1 QVOIQQSSEELVRPGASVKLSCSKAGSYFTTYMMHMKQRHGCGLEWMIGNIYPGSGITNY 60

```
QY      63 ADATKGRFITSRDNKNLTFLQNTSLRSSEDTWYYGYCARDYGAA--YMGGGTTVTVSSGGGG   12
          : | : : | : : : | | | | : ||| | | | | | | | | | | | | | | |
Dd     61 DEKKNKGIITVDISSSTAIWHLSLASEDSAVTYCCARGRGGLDVAGATTTLTVSSGGGG   12
```

```

Dy      121 SGGGSGGGSDIEITQSPALMSASGERVMTCASSV-RYNNWFOOKSGTSPRMWY 18
        |||||::||:|-|-|:-||-|-|-|-|-|-|-|-|-|-|-|-|-|-|-|-|-|-|
Db      121 SGGGSGGGSDIQMTQSSSFVSIGDRVTITCKASEDIYNRLAWYQQKPGNAPRLIS 18

```

Dy  
180 DISLSSGVFAKFSGGSGSISLTSSMEADAAITTCQ--NSSNPLTFGAGILAEK 237

Db  
181 GATLELETGPSRFSGGSGGDYTLSTSLGFEDVATYYCQGYMSTR--TFGGTLEIK 237

## RESULT 9

ID	Q92551	PRELIMINARY;	PRT;	218 AA.
----	--------	--------------	------	---------

DT 01-DEC-2001 (TREMBlere1. 19, Created)

DT 01-OCT-2003 (Tremblay, 25, Last annotation update)

OS Mus musculus (Mouse) .

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

RN	[1]
RD	OPPORTUNITIES PROVIDED BY THE

RC STRAIN=BA1B/C;  
BY D-BMOD=11010670.

RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,

### RT "Mechanism of exogenous nucleic acids and their precursors improving the formation of intestinal antibodies after irradiation in mice"

World J. Gastroenterol. 6:709-717 (2000).

RP SEQUENCE FROM N.A.

Cui D., Zeng G., Yan X., Li X., Su C.;

RT of the irradiated mice by treatment with the intestinal RNA of mice of the same strain".

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

DR HSSP; P01665; 1QNZ.  
DB SMAPT; SM00406; TGR; 1

DR	PROSITE; PS50835; IG_LIKE; 1..
ET	NON TEB 318 318

SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match	Score	DB 2;	Length
Best Local	37.5%;	608.5;	218;
Best Local	55.8%;	79.37;	

Matches 121; Conservative 33; Mismatches 55; Indels 9; Gaps 3;

QY 1 MAEVLQESGGGLVQPGGSRKLSCAASGFTFSSFGMHVVRQAPKEKLEWVAYISSGSTI 60

Db 1 MAQVKLQOSGP~~ELK~~KPGETVRISCKASGYTFTTAGM~~QWVQ~~KMPGKGLKWI~~GI~~WINTHSGVP 600

61 YYADTVKGRFTISRDNPKNTLFQMTSLRSEDVWYYCAR-DYG---AYWGCGTTVTSS 11

Db 61 KYAEFFKGRFAFSLETSASTAYLQISNLKNEDTATYFCMRWDYDGGFAYWGQTTTVSS 12

117 GCGGSGGGSDIELTQSPAIMASPGERVMTCSASSV-----RYMNFQQKSG 170



```

Query Match      33.4%; Score 542; DB 2; Length 473;
Best Local Similarity 51.7%; Pred. No. 1.6e-31;
Matches 120; Conservative 20; Mismatches 52; Indels 40; Gaps 5;

Oy 3 EYKLOESGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWVQAPKGLWVAYISSGSTIY 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 EYQLVESGGGLVQPGSGSRKLSCAASGFTFSDYGMHVRQAPKGLWVAYISSGSTIY 79
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 63 ADTVKGRFTISRDNPNKNTLFLQMTSLRSEDYVWYCARDYGA---YWGQGTIVTVSSG 118
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 ADTVKGRFTISRDNPNKNTLFLQMTSLRSEDYVWYCARDYGAELMRIDYWGQGTIVTVSSA- 138
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 119 GSGSGGGSGGGSDILTQSPALMSASRPERVMTGSSSVRYVMWFOQKSTSPKRI 178
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 139 -----KTPPSVYPLAPGCGDTGSSVTLGCLVKGLVPGQFPESVTVT----- 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 179 YPTSKLSGV---PARFSGSGGTSTYSLTISMEADATYVCOQWSSNPLT 227
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 WNSGSLSSSVHTFPALQSGLYTMSSSVTVPS-----STWPSQTVT 218
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
HVL6_MOUSE STANDARD; PRT; 136 AA.
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
RA Botwell A.L.M., Paekind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adefuogb K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants.";
RL Nature 265:299-304(1977).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL J00522; AADIS290.1; -
CC PIR: E90809; GIMS21.
CC PDB: 1IGC; X-ray; H=-.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
DR PROSITE: PS00835; IG_LIKE_1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin V region;
KW Signal.
FT SIGNAL 1 1
FT NON_TER <1 16
FT CHAIN 17 136 Ig heavy chain V region MOPC 21.
FT DOMAIN 115 119 D segment.
FT DOMAIN 120 136 JH4 segment.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (in Ref. 2).

```

```

FT CONFLICT 89 90 DN -> ND (in Ref. 2).
FT CONFLICT 115 115 W -> H (in Ref. 2).
FT CONFLICT 120 120 Y -> W (in Ref. 2).
FT STRAND 19 23
FT STRAND 26 28
FT TURN 30 31
FT STRAND 34 41
FT HELIX 45 47
FT STRAND 50 55
FT STRAND 61 67
FT TURN 69 70
FT STRAND 74 76
FT HELIX 78 80
FT STRAND 81 81
FT TURN 82 83
FT STRAND 84 89
FT TURN 90 93
FT STRAND 94 99
FT HELIX 104 106
FT STRAND 108 114
FT TURN 118 119
FT STRAND 125 126
FT STRAND 130 134
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 15071 MW; 2276398DBDF7016 CRC64;

Query Match      33.0%; Score 535; DB 1; Length 136;
Best Local Similarity 87.5%; Pred. No. 1.2e-31;
Matches 105; Conservative 5; Mismatches 4; Indels 6; Gaps 2;

Oy 3 EYKLOESGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWVQAPKGLWVAYISSGSTIY 62
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 17 DVQLVESGGGLVQPGSGSRKLSCAASGFTFSSFGMHVWVQAPKGLWVAYISSGSTIY 76
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Oy 63 ADTVKGRFTISRDNPNKNTLFLQMTSLRSEDYVWYCAR---DYGA--YWGQGTIVTVSS 116
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 77 ADTVKGRFTISRDNPNKNTLFLQMTSLRSEDYVWYCARMGNYPYAMDYWGQGTIVTVSS 136
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
KV6F_MOUSE STANDARD; PRT; 107 AA.
AC P04940;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-VI region NQ2-17.4.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RX MEDLINE=83271467; PubMed=6877353;
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -----
CC -I- FUNCTION: Anti-2-phenyl oxazalone (PROX) Antibody.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: K00735; AAA38680.1; -
CC HSSP: P01679; 2FBJ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.

```

DR SMART; SM00406; IG; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KW Hybridoma; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 33 Complementarity-determining-1.  
 FT DOMAIN 34 48 Framework-2.  
 FT DOMAIN 49 55 Complementarity-determining-2.  
 FT DOMAIN 56 87 Framework-3.  
 FT DOMAIN 88 96 Complementarity-determining-3.  
 FT DOMAIN 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11561 MW; 6F694284ECFA68B6 CRC64;

Query Match 31.3%; Score 507; DB 1; Length 107;  
 Best Local Similarity 90.6%; Pred. No. 1.1e-29;  
 Matches 96; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 133 IEITQSPAINASPGERVMTCSASSSVRYMNFQOKSGTSPKRWYDTSKLSGVPARF 192  
 DB 2 IVLTQSPAINASPGQKVTMTCSASSSVSYMHVYQOKSGTSPKRWYDTSKLSGVPARF 61  
 QY 193 SGGSGSTSYSLTSSMEADPAATYYCOQSSNPLTFGAGTKLEIKR 238  
 DB 62 SGGSGSTSYSLTSSMEADPAATYYCOQSSNPLTFGAGTKLEIKR 107

## RESULT 14

KV6H\_MOUSE STANDARD; PRT; 107 AA.

AC P04942;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-VI region HQ5-61.1.2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=3271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
 RT "mRNA sequences define an unusually restricted IGH response to 2-phenylloxazalone and its early diversification.";  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.  
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 CC EMBL; K00739; AAA38684.1; -  
 DR HSSP; P01679; 2PBJ  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KW Hybridoma; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 33 Complementarity-determining-1.  
 FT DOMAIN 34 48 Framework-2.  
 FT DOMAIN 49 55 Complementarity-determining-2.  
 FT DOMAIN 56 87 Framework-3.  
 FT DOMAIN 88 96 Complementarity-determining-3.  
 FT DOMAIN 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON\_TER 107 107

QY 133 IEITQSPAINASPGERVMTCSASSSVRYMNFQOKSGTSPKRWYDTSKLSGVPARF 192  
 DB 2 IVLTQSPAINASPGQKVTMTCSASSSVSYMHVYQOKSGTSPKRWYDTSKLSGVPARF 61  
 QY 193 SGGSGSTSYSLTSSMEADPAATYYCOQSSNPLTFGAGTKLEIKR 238  
 DB 62 SGGSGSTSYSLTSSMEADPAATYYCOQSSNPLTFGAGTKLEIKR 107

SQ SEQUENCE 107 AA; 11605 MW; CA6C4284EFCB550 CRC64;

Query Match 31.2%; Score 506; DB 1; Length 107;  
 Best Local Similarity 90.6%; Pred. No. 1.3e-29;  
 Matches 96; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 133 IEITQSPAINASPGERVMTCSASSSVRYMNFQOKSGTSPKRWYDTSKLSGVPARF 192  
 DB 2 IVLTQSPAINASPGQKVTMTCSASSSVSYMHVYQOKSGTSPKRWYDTSKLSGVPARF 61  
 QY 193 SGGSGSTSYSLTSSMEADPAATYYCOQSSNPLTFGAGTKLEIKR 238  
 DB 62 SGGSGSTSYSLTSSMEADPAATYYCOQSSNPLTFGAGTKLEIKR 107

## RESULT 15

KV6I\_MOUSE STANDARD; PRT; 107 AA.

AC P04943;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG kappa chain V-VI region HQ6-8.3.1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=3271467; PubMed=6877353;  
 RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;  
 RT "mRNA sequences define an unusually restricted IGH response to 2-phenylloxazalone and its early diversification.";  
 RL Nature 304:320-324(1983).  
 CC -1- FUNCTION: Anti-2-phenyl oxazalone (PHOX) Antibody.  
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 CC EMBL; K00740; AAA38685.1; -  
 DR HSSP; P01679; 2PBJ  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IG; 1.  
 DR PROSITE; PSS0835; IG LIKE; 1.  
 KW Hybridoma; Immunoglobulin V region.  
 FT DOMAIN 1 23 Framework-1.  
 FT DOMAIN 24 33 Complementarity-determining-1.  
 FT DOMAIN 34 48 Framework-2.  
 FT DOMAIN 49 55 Complementarity-determining-2.  
 FT DOMAIN 56 87 Framework-3.  
 FT DOMAIN 88 96 Complementarity-determining-3.  
 FT DOMAIN 97 106 Framework-4.  
 FT DISULFID 23 87 By similarity.  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11572 MW; 6F694824EFC0CB6 CRC64;

Query Match 30.9%; Score 502; DB 1; Length 107;  
 Best Local Similarity 89.6%; Pred. No. 2.5e-29;  
 Matches 95; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 133 IEITQSPAINASPGERVMTCSASSSVRYMNFQOKSGTSPKRWYDTSKLSGVPARF 192  
 DB 2 IVLTQSPAINASPGQKVTMTCSASSSVSYMHVYQOKSGTSPKRWYDTSKLSGVPARF 61  
 QY 193 SGGSGSTSYSLTSSMEADPAATYYCOQSSNPLTFGAGTKLEIKR 238  
 DB 62 SGGSGSTSYSLTSSMEADPAATYYCOQSSNPLTFGAGTKLEIKR 107

Db 62 SSGSATSYSLITSMQAEADATYCCQMSNPFTGAGTKLEKR 107

Search completed: June 23, 2005, 05:52:29  
Job time : 86 secs



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OM protein - protein search, using sw model

Run on: June 23, 2005, 05:50:26 ; Search time 77 Seconds  
(without alignments)  
1587.224 Million cell updates/sec

Title: US-09-403-882a-2

Perfect score: 1622  
Sequence: 1 MAEVLKQSGGLVQPGGSR.....VLTITLITLIMWKKER 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004as:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1622	100.0	316	2	AAV32086
2	1319	81.3	255	3	AAAB11398
3	1319	81.3	255	4	AAAB74199
4	1319	81.3	255	4	AAAB70769
5	1319	81.3	255	4	AAAB72020
6	1237	76.3	241	6	ABR62010
7	1227	75.6	241	5	AAAB48925
8	1194	73.6	236	2	AAAB2842
9	1185	73.1	240	2	AAAB68613
10	1097.5	67.7	223	2	AAAB32841
11	1008	62.1	580	2	AAAB30217
12	1001	61.7	556	2	AAAB30218
13	976.5	60.2	237	7	AAAB38657
14	970.5	59.6	268	3	AAAB4973
15	967.5	59.6	268	3	AAAB4973
16	964.5	59.5	284	2	AAAB5569
17	959	58.1	281	2	AAAB5569
18	954	58.1	281	2	AAAB5569
19	939	57.9	234	2	AAAB4819
20	938.5	57.9	235	2	AAAB4819
21	937.5	57.8	272	8	ADAB19054
22	937	57.8	258	2	AAAB0221
23	935.5	57.7	234	2	AAAB20442
24	934.5	57.6	233	4	AAAB5715
25	928.5	57.2	282	6	ABJ19276

26	927	57.2	291	8	ADAB06992
27	926	57.1	287	8	ADAB06988
28	921.5	56.8	244	8	ADAB75290
29	919	56.7	553	2	AAAB11508
30	919	56.7	553	2	AAAB73223
31	919	56.7	553	4	AAAB1960
32	919	56.7	553	4	AAAB5455
33	917.5	56.6	269	8	ADAB17525
34	913	56.3	242	6	ABR62132
35	913	56.3	242	6	ADAB91209
36	912	56.2	342	8	ADAB75289
37	907	55.9	353	2	AAAB06273
38	906.5	55.9	237	5	ABAB46093
39	906.5	55.9	237	7	ADAB69920
40	906.5	55.9	253	2	AAAB90225
41	903.5	55.7	237	5	ABAB46009
42	903.5	55.7	237	5	ADAB68836
43	900.5	55.5	237	5	ABAB46103
44	900.5	55.5	237	5	ABAB45994
45	900.5	55.5	237	7	ADAB69930

## ALIGNMENTS

RESULT 1	AAV32086	AAV32086 standard; protein; 316 AA.
ID	AAV32086	
XX	AAV32086	
AC	AAV32086	
DT	17-JAN-2000 (first entry)	
XX		
DE	Single chain antibody used in probe detection.	
XX		
KM	Single chain antibody; scab; sfv; spectroscopic probe.	
XX		
OS	Unidentified	
XX		
PD	MO9951986-A1.	
XX	14-OCT-1998	
XX		
PF	08-APR-1999; 99WC-US007847.	
XX		
PR	08-APR-1998; 98US-008118P.	
PR	09-APR-1998; 98US-0081340P.	
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX		
PI	Farinas J;	
XX		
DR	WPI, 1999-611066/52.	
XX	N-PDB; AA220266.	
PT	Localizing probes to specific sites in cells that express single-chain	
PT	antibody reactive with probe-1ligand conjugate, particularly for detecting	
PT	post-translational modification and its modulators.	
XX		
PS	Claim 5; Page 47-48; 69pp; English.	
XX		
CC	The present sequence represents a single chain antibody (scab) that has 2	AdAB06992 Human EFG
CC	c-myc epitopes. The scab is used in claimed methods for localizing a	AdAB06988 Human EFG
CC	probe and for detecting a post-translational activity in a cell, and is	AdAB75290 Immunoglo
CC	expressed by a claimed transgenic non-human animal. The invention	AAAB11508 Single ch
CC	provides methods and reagents for targeting probes to selected cellular	AAAB73223 H22-anti-
CC	locations through the expression of specific binding partners (such as	AAAB1960 Bispectifi
CC	scabs) within a cell, and for creating assays for post-translational	AAAB5455 Bispectifi
CC	activities. The invention allows the monitoring of the location of such	AdAB17525 Antno act
CC	intracellular, specific binding partners over time and in response to	AdAB91209 Single ch
CC	stimuli, such as test chemicals. Spectroscopic probes can be used to	AdAB75289 Immunoglo
CC	screen a test chemical for activity. The invention also includes cells	AAAB06273 Anti Fc a
CC	and transgenic organisms comprising the intracellular specific binding	ABAB46093 Human Bly
CC		AdAB69920 Single ch
CC		AAAB90225 Anti-B7.1
CC		ABAB46009 Human Bly
CC		AdAB68836 Single ch
CC		ABAB46103 Human Bly
CC		ABAB45994 Human Bly
CC		AdAB69930 Single ch

CC partner, where the specific binding partner can bind with the  
 CC spectroscopic probe/ligand conjugate. scabs can be expressed within the  
 CC cell and can be designed to bind a wide variety of spectroscopic probes,  
 CC including small molecules that have better (and more diverse)  
 CC spectroscopic properties than green fluorescent protein

XX Sequence 316 AA;

Query Match 100.0%; Score 1622; DB 2; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-108;  
 Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAEVLQESGGGLVOPGSRKLSCAASGTFSSFGMHVWROAPEKLEWAVYISGSSSTI 60  
 DB 1 MAEVLQESGGGLVOPGSRKLSCAASGTFSSFGMHVWROAPEKLEWAVYISGSSSTI 60  
 QY 61 YVADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYVCARDYGAYWGQTTVTSSGGGG 120  
 DB 61 YVADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYVCARDYGAYWGQTTVTSSGGGG 120  
 QY 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMWFQKSGTSPKRWIYD 180  
 DB 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMWFQKSGTSPKRWIYD 180  
 QY 181 TSKLSSGVPARFSGSGSTSYSLTSSMEABDAATYYCOQSSNPLTFGAGTKLELKRAA 240  
 DB 181 TSKLSSGVPARFSGSGSTSYSLTSSMEABDAATYYCOQSSNPLTFGAGTKLELKRAA 240  
 QY 241 AEOKLISEEDLNGAVDEOKLISEEDLNAYGODTQEVIVPHSLPFVVVYISAIIALVLT 300  
 DB 241 AEOKLISEEDLNGAVDEOKLISEEDLNAYGODTQEVIVPHSLPFVVVYISAIIALVLT 300  
 QY 301 IISLIILMLMOKKPR 316  
 DB 301 IISLIILMLMOKKPR 316

RESULT 2  
 AAB11398

ID AAB11398 standard; protein; 255 AA.

AC AAB11398;

DT 22-FEB-2001 (first entry)

DE E. coli expression plasmid pUBS520-ScFvOX encoded protein.

XX Eukaryotic protein; protease; interferon; antibody; hormone;  
 KW disulfide bridge.

XX Escherichia coli.

OS Synthetic.

XX EPI048732-A1.

PN 02-NOV-2000.

PD 26-APR-1999; 99EP-00107412.

PF 26-APR-1999; 99EP-00107412.

PR (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

DR N-PSDB; AAC66074.

XX Preparation of water-soluble eukaryotic polypeptides with disulfide  
 PT bridges e.g. rPA, comprises cultivation of prokaryotic cells in the  
 PT presence of arginine or amide compound.

XX Example 6; Page 22-23; 40pp; German.

XX This invention describes a novel preparation of a water-soluble,  
 CC

CC naturally occurring eukaryotic polypeptide containing two or more  
 CC cysteine units bound via a disulfide bridge which comprises cultivation  
 CC of prokaryotic cells in the presence of arginine or an amide compound.  
 CC The method is useful for the preparation of eukaryotic proteins e.g.  
 CC proteases, interferons, protein hormones, antibodies or antibody  
 CC fragments (e.g. a single chain Fv fragment that binds to thyroid  
 CC stimulating hormone). It is especially useful for preparing proteins with  
 CC more than five disulfide bridges, e.g. recombinant plasmidogen activator  
 CC (rPA). The technique is simple and does not require in vitro after-  
 CC treatment, such as the removal of inclusion bodies, reduction or  
 CC naturation

XX Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 3; Length 255;  
 Best Local Similarity 99.2%; Pred. No. 1.2e-86;  
 Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVLQESGGGLVOPGSRKLSCAASGTFSSFGMHVWROAPEKLEWAVYISGSSSTI 60  
 DB 1 MAEVLQESGGGLVOPGSRKLSCAASGTFSSFGMHVWROAPEKLEWAVYISGSSSTI 60  
 QY 61 YVADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYVCARDYGAYWGQTTVTSSGGGG 120  
 DB 61 YVADTVKGRFTISRDNPKNTLFLQMTSLRSEDTVMYVCARDYGAYWGQTTVTSSGGGG 120  
 QY 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMWFQKSGTSPKRWIYD 180  
 DB 121 SGGGGSGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMWFQKSGTSPKRWIYD 180  
 QY 181 TSKLSSGVPARFSGSGSTSYSLTSSMEABDAATYYCOQSSNPLTFGAGTKLELKRAA 240  
 DB 181 TSKLSSGVPARFSGSGSTSYSLTSSMEABDAATYYCOQSSNPLTFGAGTKLELKRAA 240  
 QY 241 AEOKLISEEDLNGA 254  
 DB 241 AEOKLISEEDLNGA 254

RESULT 3  
 AAB74199

ID AAB74199 standard; protein; 255 AA.

AC AAB74199;

DT 29-MAY-2001 (first entry)

DE PelB-scFvOxazolone fusion protein.

XX Molecular chaperone; PelB signal sequence; scFvOxazolone.

XX Unidentified.

XX EPI077262-A1.

PN 21-FEB-2001.

PD 24-JUL-2000; 2000EP-00115839.

PF 29-JUL-1999; 99EP-00114811.

PR (HOFF) HOFFMANN LA ROCHE & CO AG F.

PA Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;

DR MPI; 2001-246712/26.

DR N-PSDB; AAF77806.

XX Producing naturally folded eukaryotic proteins e.g. antibodies,  
 PT interferon, hormones or proteases that contain two or several cysteines  
 PT linked by disulfide bridges comprises co-expression of a molecular  
 PT chaperone.

XX

PS Disclosure; Page 19; 35pp; English.

XX  
XX  
CC The present invention relates to a method for production of a naturally  
CC folded eukaryotic protein containing two or more cysteines linked by  
CC disulfide bridges. The method comprises co-expression and secretion into  
CC the periplasm of a molecular chaperone via an expression vector coding  
CC for the chaperone. The expression vector also encodes a signal sequence.  
CC The method is useful for producing a naturally folded eukaryotic protein  
CC such as an antibody, antibody fragment, interferon, protein hormone or a  
CC process containing two or several cysteines linked by disulfide bridges.  
CC The present sequence is a fusion protein composed of the pelb signal  
CC sequence and ScFvOxazoln. This sequence was used in the method of the  
CC present invention  
XX  
SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;  
Best Local Similarity 99.2%; Pred. No. 1.2e-86;  
Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MAEVKIQESGGGLVOPGSRKLSCAASGFTFSFGHMYRQAPKGLMVAIYSSGSSSTI 60  
1 MAEVKIQESGGGLVOPGSRKLSCAASGFTFSFGHMYRQAPKGLMVAIYSSGSSSTI 60  
61 YVADTVKGRFTISRDPKNTLFLQMTSLRSEDTVMYICARDYGAVYGQGTIVTVSSGGGG 120  
61 YVADTVKGRFTISRDPKNTLFLQMTSLRSEDTVMYICARDYGAVYGQGTIVTVSSGGGG 120  
121 SGGGGSGGGGSDIELTQSPAIMSASPERVMTCSASSSVRYNMWFOOKSGTSPKMIYD 180  
121 SGGGGSGGGGSDIELTQSPAIMSASPERVMTCSASSSVRYNMWFOOKSGTSPKMIYD 180  
181 TSKLSSGVPAFPSSGSGSTSYSLTSSMEADPAATYYCOOMSNPLTFAGTLELKRRA 240  
181 TSKLSSGVPAFPSSGSGSTSYSLTSSMEADPAATYYCOOMSNPLTFAGTLELKRRA 240  
241 AEOKLISEEDLNGA 254  
241 AEOKLISEEDLNGA 254

RESULT 4  
AAB70769 standard; protein; 255 AA.

XX  
XX  
AC AAB70769;

DT 18-MAY-2001 (first entry)

DE Expression plasmid pUBS520-ScFvOx protein.

KW Chaperone protein; periplasm; antibody production; protein production;  
KW Interferon production; protease production.

OS Escherichia coli.  
OS Synthetic.

PN EP1077263-A1.

PD 21-FEB-2001.

PF 29-JUL-1999; 99EP-00114811.

PR 29-JUL-1999; 99EP-00114811.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX WPI; 2001-204356/21.

DR N-PSDB; AAF61193.

PT Preparation of naturally folded eukaryotic proteins, e.g. antibodies, by  
PT simultaneous expression of a chaperone protein, allows simple recovery  
PT from periplasm or medium.

XX  
XX  
PS Disclosure; Page 20-21; 36pp; German.

CC This invention describes a novel method for preparing a naturally folded  
CC eukaryotic polypeptide (I) that contains two or more disulfide-bridged  
CC Cys residues by culturing prokaryotic cells that contain an expression  
CC vector for (I) including a prokaryotic signal sequence at its N-terminus  
CC and a nucleic acid (II) that secretes a chaperone protein (III) into the  
CC periplasm. (II) is secreted into the periplasm or medium; the signal  
CC peptide is then cleaved and (I) isolated from the periplasm or medium.  
CC The method is used for production of antibody, interferon, protein  
CC hormone or protease. Expression of (III) increases the yield of (I). The  
CC method is simple and eliminates time-consuming in vitro processing  
CC operations such as dissolution of inclusion bodies, reduction and  
CC refolding. (III) protects (I) against agglomeration and promotes their  
CC natural conformation

SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;  
Best Local Similarity 99.2%; Pred. No. 1.2e-86;  
Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MAEVKIQESGGGLVOPGSRKLSCAASGFTFSFGHMYRQAPKGLMVAIYSSGSSSTI 60  
1 MAEVKIQESGGGLVOPGSRKLSCAASGFTFSFGHMYRQAPKGLMVAIYSSGSSSTI 60  
61 YVADTVKGRFTISRDPKNTLFLQMTSLRSEDTVMYICARDYGAVYGQGTIVTVSSGGGG 120  
61 YVADTVKGRFTISRDPKNTLFLQMTSLRSEDTVMYICARDYGAVYGQGTIVTVSSGGGG 120  
121 SGGGGSGGGGSDIELTQSPAIMSASPERVMTCSASSSVRYNMWFOOKSGTSPKMIYD 180  
121 SGGGGSGGGGSDIELTQSPAIMSASPERVMTCSASSSVRYNMWFOOKSGTSPKMIYD 180  
181 TSKLSSGVPAFPSSGSGSTSYSLTSSMEADPAATYYCOOMSNPLTFAGTLELKRRA 240  
181 TSKLSSGVPAFPSSGSGSTSYSLTSSMEADPAATYYCOOMSNPLTFAGTLELKRRA 240  
241 AEOKLISEEDLNGA 254  
241 AEOKLISEEDLNGA 254

RESULT 5  
AAY72020 standard; protein; 255 AA.

XX  
XX  
AC AAY72020;

DT 28-MAR-2001 (first entry)

DE E. carotovora pelB-scFvOx fusion protein encoded by pUBS520-p1N-scFvOx.

KW Secreted protein; chaperone; interferon; protease; hormone;  
KW naturally folded protein; lac promoter; DnaJ; heat shock protein; HSP;  
KW pectate lyase B; pelB; hapten; single-chain Fv-fragment Oxazoln;  
KW ScFvOxazoln; fusion protein; thyroid stimulating hormone; TSH.

XX Pectobacterium carotovorum.

OS Undefined.

OS Chimeric.

PN EP1054063-A2.

PD 22-NOV-2000.

PF 19-APR-2000; 2000EP-00108505.

PR 26-APR-1999; 99EP-00107412.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Ambrosius D, Rudolph R, Schaeffner J, Schwarz E;  
XX WPI; 2001-033777/05.  
DR N-PSDB; AAD02212.  
XX  
XX  
XX Producing water-soluble, naturally folded, and secreted eukaryotic  
PT polypeptide, involves culturing prokaryotic cells containing an  
PT expression vector encoding the polypeptide in the presence of arginine or  
PT a specific compound.

Example 6; Page 22-23; 35pp; English.

XX The patent discloses a method for the production of a water-soluble,  
CC naturally folded and secreted eukaryotic proteins in prokaryotic cells.  
CC The method involves culturing the prokaryotic cells, containing an  
CC expression vector encoding the desired protein and the prokaryotic signal  
CC sequence, in the presence of an additive, e.g., L-arginine. The signal  
CC sequence mediates the secretion of the desired protein into the  
CC periplasm, where folding of the protein takes place. The prokaryotic cell  
CC also contains an expression vector encoding a molecular chaperone, e.g.,  
CC DnaK and heat shock protein 25 (HSP25). The simultaneous co-  
CC overexpression and co-secretion of molecular chaperones in the periplasm  
CC improves the yield of functionally folded protein. The above method  
CC recombinantly produces a high yield of eukaryotic secreted proteins in  
CC prokaryotes. The method is useful for producing eukaryotic proteins such  
CC as an antibody, antibody fragment, interferon, protein hormone or a  
CC protease. The present sequence is an Erwinia carotovora pectate lyase B  
CC (PelB) signal sequence-scFvOx fusion protein encoded by PUBS520-PIN-  
CC scFvOx. The plasmid, pUBS520-PIN-scFvOx, also comprises the lac promoter.  
CC The single-chain Fv-fragment, which is directed against the hapten  
CC oxazolone (ScFvOxazolone), is an antibody fragment against thyroid  
CC stimulating hormone (TSH). The co-expression of ScFvOx which has no  
CC chaperone properties is used as a negative control  
XX  
SQ Sequence 255 AA;

Query Match 81.3%; Score 1319; DB 4; Length 255;  
Best Local Similarity 99.2%; Pred. No. 1.2e-86;  
Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVLKQESGGGLVOPGGSRKLSCAASGFTFSSFGMHWROAPEKGLWVAYISSGSSSTI 60  
Db 1 MMEVLKQESGGGLVOPGGSRKLSCAASGFTFSSFGMHWROAPEKGLWVAYISSGSSSTI 60  
QY 61 YYADTVKGRFTTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTIVVSSGGGG 120  
Db 61 YYADTVKGRFTTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTIVVSSGGGG 120  
QY 121 SGGGSGGGGSDIELTQSPAIMSASPERVTMTCSASSSVRYMNMFOQSGTSPKRWIYD 180  
Db 121 SGGGSGGGGSDIELTQSPAIMSASPERVTMTCSASSSVRYMNMFOQSGTSPKRWIYD 180  
QY 181 TSKLSSGVPARFSGSGSGTYSLTITSSMEADAAATYYCOQWSSNPLTFAGTKLELKRAA 240  
Db 181 TSKLSSGVPARFSGSGSGTYSLTITSSMEADAAATYYCOQWSSNPLTFAGTKLELKRAA 240  
QY 241 AEQKLISEEDLNGA 254  
Db 241 AEQKLISEEDLNGA 254

RESULT 6  
ABR62010  
ID ABR62010 standard; protein; 241 AA.

XX ABR62010;

XX 03-OCT-2003 (first entry)

XX Single-chain (scFv) antibody.

XX Transgenic; biomolecule; ATP; ADP; cyrostatic; virucide; gene therapy;  
KM Antisense therapy; scFv; antibody.

XX  
OS Synthetic.  
XX  
XX EPI321524-A1.  
XX  
XX 25-JUN-2003.  
XX  
XX 19-DEC-2001; 2001EP-00130319.  
XX  
XX 19-DEC-2001; 2001EP-00130319.  
XX  
XX  
XX (DUEB/) DUEBING K.  
XX  
XX Mahn A, Hanke S, Petersch D;  
XX  
XX WPI; 2003-543829/52.  
XX  
XX N-PSDB; ACC84876.  
XX  
XX  
XX Increasing the content of transgene-coded biomolecules in a plant or  
XX animal, useful for producing proteins for diagnosing, preventing and/or  
XX treating viral diseases and cancer, comprises changing the distribution  
XX of ATP and/or ADP.

PS Example 2; Fig 2; 18pp; English.

XX The invention relates to increasing the content of one or more transgene-  
CC coded biomolecules in an organism and involves changing the distribution  
CC of ATP and/or ADP in cells of the organism. The yield of transgenic  
CC molecules in host cells is often insufficient for industrial production.  
CC The method increases the yield of transgenic molecules in animal and  
CC plant host cells, therefore facilitating their production on an  
CC industrial scale. The proteins produced by the method are useful for  
CC diagnosing, preventing and/or treating viral diseases and cancer. The  
CC present sequence represents a single-chain (scFv) antibody, used to  
CC exemplify the increase in the expression of scFv antibodies in transgenic  
XX potato tubers  
XX  
SQ Sequence 241 AA;

Query Match 76.3%; Score 1237; DB 6; Length 241;  
Best Local Similarity 97.9%; Pred. No. 8.5e-81;  
Matches 235; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AEVLKQESGGGLVOPGGSRKLSCAASGFTFSSFGMHWROAPEKGLWVAYISSGSSSTI 61  
Db 2 ADVQLVESGGGLVOPGGSRKLSCAASGFTFSSFGMHWROAPEKGLWVAYISSGSSSTI 61  
QY 62 YADTVKGRFTTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTIVVSSGGGG 121  
Db 62 YADTVKGRFTTISRDNPKNTLFLQMTSLRSEDTVMYYCARDYGAYWGQGTIVVSSGGGG 121  
QY 122 GGGGSGGGGSDIELTQSPAIMSASPERVTMTCSASSSVRYMNMFOQSGTSPKRWIYD 181  
Db 122 GGGGSGGGGSDIELTQSPAIMSASPERVTMTCSASSSVRYMNMFOQSGTSPKRWIYD 181  
QY 182 SKLSSGVPARFSGSGSGTYSLTITSSMEADAAATYYCOQWSSNPLTFAGTKLELKRAA 241  
Db 182 SKLSSGVPARFSGSGSGTYSLTITSSMEADAAATYYCOQWSSNPLTFAGTKLELKRAA 241

RESULT 7  
AAM48925  
ID AAM48925 standard; protein; 241 AA.

XX AAM48925;

XX 03-MAY-2002 (first entry)

XX scFv antibody.

XX Ketone binding protein; oxazole; pathogen resistance; virucide;  
KM fungicide; antibacterial; scFv antibody.

```

OS Unidentified.
XX
XX Key Location/Qualifiers
XX Misc-difference 137 /note= "encoded by CAG"
XX FT Misc-difference 201 /note= "encoded by TAC"
XX FT
XX WO200204020-A2.
XX
XX PD 17-JAN-2002.
XX
XX PF 17-MAY-2001; 2001WO-DE001916.
XX
XX PR 12-JUL-2000; 2000DE-01033750.
XX
XX PA (MPBC-) MPB COLOGNE GMBH.
XX
XX PI Duering K, Brinkmann O;
XX
XX DR MPI; 2002-154868/20.
XX DR N-PSDB; AAK98639.
XX
XX PT Imparting pathogen resistance to plants and animals, comprises using a
XX PT polypeptide that binds to an oxazole-derived ketone, optionally expressed
XX PT from nucleic acid.
XX
XX PS Example 3; Fig 1; 20pp; German.
XX
XX CC The present invention relates to the use of a polypeptide that binds a
XX CC ketone derived from oxazole for generating pathogen resistance in an
XX CC organism. This can be used to impart resistance to pathogens (bacteria,
XX CC fungi or viruses) to a wide range of plants (e.g. cereals, sugar beet,
XX CC tobacco etc.), humans, farm animals and pets. Exemplified are activities
XX CC against Phytophthora infestans and Erwinia carotovora in potatoes and
XX CC Stephylococcus aureus in mice. The present sequence is a sc-Fv antibody,
XX CC which is capable of binding 2-phenyloxazol-5-one
XX
XX SQ Sequence 241 AA;
XX
XX Query Match 75.6%; Score 1227; DB 5; Length 241;
XX Best Local Similarity 97.1%; Pred. No. 4.5e-80;
XX Matches 234; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 MAEVTLQESGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLEWVAIYSSGSSSTI 60
XX DB 1 MADVLVBSGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLEWVAIYSSGSSSTI 60
XX
XX QY 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYTCARDYGAYWGCGTTVYSSGGG 120
XX DB 61 YYADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYTCARDYGAYWGCGTTVYSSGGG 120
XX
XX QY 121 SGGGSGGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMMWFQOKSGTSPKRWIYD 180
XX DB 121 SGGGSGGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMMWFQOKSGTSPKRWIYD 180
XX
XX QY 181 TSKLSSGVPARFSSGSGSTYSILTSSMAEDAAATYTCQOMSSNPLTFGAGTKLEKRAA 240
XX DB 181 TSKLSSGVPARFSSGSGSTYSILTSSMAEDAAATYTCQOMSSNPLTFGAGTKLEKRAA 240
XX
XX QY 241 A 241
XX DB 241 A 241
XX
XX RESULT 8
XX ID AAR32842
XX AAR32842 standard; protein; 236 AA.
XX
XX AC AAR32842;
XX
XX DT 25-MAR-2003 (revised)
XX DT 19-JUN-1993 (first entry)

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XX DE VH NQ10/12.5-VK NQ10/12.5 linked peptide sequences #2.
XX
XX KW Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;
XX KW lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;
XX KW in-cell PCR; cloning; polymorphic; TCR V; antiphenyloxazolone; hybridoma;
XX KW NQ2/12.4; NQ10/12.5.
XX
XX OS Synthetic.
XX
XX XX Key Location/Qualifiers
XX FH Region 1..115
XX FT /label= VH_NQ10/12.5
XX FT Peptide 116..129
XX FT /note= "Linker peptide"
XX FT Region 130..236
XX FT /label= Vkapppa_NQ10/12.5
XX
XX PN WO9303151-A1.
XX
XX PD 18-FEB-1993.
XX
XX PF 10-AUG-1992; 92WO-GB001483.
XX
XX PR 10-AUG-1991; 91GB-00017352.
XX PR 11-JUN-1992; 92GB-00012419.
XX
XX PA (MED1-) MEDICAL RES COUNCIL.
XX
XX PI Embleton MJ, Gorochev G, Jones PT, Winter GP;
XX
XX DR MPI; 1993-076508/09.
XX DR N-PSDB; AAG37461.
XX
XX PT Treatment of cell populations, partic. hybridomas - to link together
XX PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis.
XX
XX PS Disclosure; Fig 4; 72pp; English.
XX
XX CC The sequences given in AAR32840-43 show the mature heavy chain VH domains
XX CC and the VK light chain genes of the antiphenyloxazolone hybridomas
XX CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-
XX CC cell PCR. The cDNA encoding these peptides was synthesised using forward
XX CC primers annealing to the Ck gene and the JH segment, followed by assembly
XX CC with linker primers, VH back primers based on the VH3 leader sequence and
XX CC a forward Ck primer nested in respect to the primer used for cDNA. The
XX CC assembled product within the cells is then amplified with nested primers
XX CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.
XX CC In-cell PCR may be used to determine gene linkage analysis, particularly
XX CC for the cloning of gene combinations that are polymorphic within a
XX CC population of cells, such as the rearranged genes for Ig or TCR V
XX CC regions. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 236 AA;
XX
XX Query Match 73.6%; Score 1194; DB 2; Length 236;
XX Best Local Similarity 96.2%; Pred. No. 1e-77; 5; Indels 0; Gaps 0;
XX Matches 226; Conservative 4; Mismatches 5;
XX
XX QY 3 EYKLOESGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLEWVAIYSSGSSSTIY 62
XX DB 1 DYOVLBSGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLEWVAIYSSGSSSTIY 60
XX
XX QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYTCARDYGAYWGCGTTVYSSGGGSG 122
XX DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTMYTCARDYGAYWGCGTTVYSSAGGSGG 120
XX
XX QY 123 GGGSGGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMMWFQOKSGTSPKRWIYDTS 182
XX DB 121 GGGSGGGGSDIELTQSPAIMSASPGERVMTCSASSSVRYMMWFQOKSGTSPKRWIYDTS 180
XX
XX QY 183 KLSGVPARFSSGSGSTYSILTSSMAEDAAATYTCQOMSSNPLTFGAGTKLEK 237
XX

```

Db 181 KLSSGVPARFSGSGSTSYSLTSSMEADATYYCOQMSNPLTFGAGTKLELK 235

RESULT 9  
AAR68613  
ID AAR68613 standard; protein; 240 AA.  
XX  
AC AAR68613;  
XX  
DT 25-MAR-2003 (revised)  
DT 13-SEP-1995 (first entry)  
XX  
DE Single chain antibody (scFv) which binds to phenylloxazolone.  
XX  
KM Genetic selection; ligand binding protein; cholera toxin; promoter;  
KM detection; selection; beta galactosidase; lac; transmembrane domain;  
KM regulatory domain; de.  
XX  
OS Synthetic.  
XX  
DE AAR319296-A1.  
XX  
PD 15-DEC-1994.  
XX  
PF 10-JUN-1993; 93DE-04319236.  
XX  
PR 10-JUN-1993; 93DE-04319236.  
XX  
PA (BEHM) BEHRINGWERKE AG.  
XX  
PI Fritz H, Hennecke F, Kolmar H;  
XX  
DR WPI; 1995-023689/04.  
DR N-PSDB; AAQ80468.  
XX  
PT Genetic selection of ligand binding proteins in microorganisms - by  
PT extracytoplasmic protein presentation, then use of ligand binding to  
PT express a detectable or selectable function.  
XX  
PS Example 2.2; Fig 4; 25pp; German.  
XX  
CC Genetic selection in microorganisms, for ligand binding proteins (LBP)  
CC comprises: extracytoplasmic presentation of LBP and; using the signal of  
CC ligand binding (by signal transduction on the biosynthetic machinery of  
CC the microorganisms) to express a detectable or selectable function.  
CC Microorganisms for this process include a genetically stable  
CC detection/selection and are transformed with a replicon encoding a fusion  
CC protein consisting of the LBP, a transmembrane helix and regulatory  
CC domain. The detection/selection function is expression of a beta-  
CC galactosidase gene, integrated into the chromosome and under the control  
CC of the ctx (cholera toxin) promoter. The transmembrane helix is taken  
CC from the toxR gene. Four primers (AAQ80457-60) were used in the  
CC construction of the plasmid pKTXscFv. The primers described in AAQ80457  
CC -58 were used to amplify variable heavy chain sequence of the single  
CC chain antibody NQ10.12.5 and those described in AAQ80459-60 were used to  
CC amplify the corresponding light chain sequence from the same antibody.  
CC The amplified sequences were cloned into the plasmid pKTXscFv (See  
CC AAQ80454-56 for details) to create a toxR-scFv fusion gene. This sequence  
CC is the single chain antibody (scFv). (Updated on 25-MAR-2003 to correct  
CC PN field.)  
XX  
SQ Sequence 240 AA;  
XX  
Query Match 73.1%; Score 1185; DB 2; Length 240;  
Best Local Similarity 95.7%; Pred. No. 4.6e-77;  
Matches 225; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

4 VKLQSGSGGLVQPGSSRLKSCAASGFTSSFGMWVROAPEKGLMVAIVISSGSSITYYA 63  
6 VOLVELGGGFGVQPGSSRLKSCAASGFTSSFGMWVROAPEKGLMVAIVISSGSSITYYA 65  
64 DTVKGRFTISDNPKNITFLQMTSLRSBDTWYVYCARPYGAVWGQGLTVYSSGGGSGG 123

Db 66 DTVKGRFTISDNPKNITFLQMTSLRSBDTWYVYCARPYGAVWGQGLTVYSSGGGSGG 125

QY 124 GSGGGGSDIELTQSPALMSASPGERYVTMTCSASSVRYNMVFOOKSGTSPKRWIYDTSK 183  
Db 126 GSGGGGSDIYLTQSPALMSASPGERYVTMTCSASSVRYNMVFOOKSGTSPKRWIYDTSK 185

QY 184 LSSGVPARFSGSGSTSYSLTSSMEADATYYCOQMSNPLTFGAGTKLELK 238  
Db 186 LSSGVPARFSGSGSTSYSLTSSMEADATYYCOQMSNPLTFGAGTKLELK 240

RESULT 10  
AAR32841  
ID AAR32841 standard; protein; 223 AA.  
XX  
AC AAR32841;  
XX  
DT 25-MAR-2003 (revised)  
DT 19-JUN-1993 (first entry)  
XX  
DE VH NQ10/12.5-VK NQ10/12.5 linked peptide sequences.  
XX  
KM Primer; human; immunoglobulin; Ig; variable region; VH; VL; Ck; JH;  
KM lymphocyte; vector; soluble; antibody; phage; linker; back; VH3; nested;  
KM in-cell PCR; cloning; polymorphic; TCR V; antiphenylloxazolone; hybridoma;  
KM NQ2/12.4; NQ10/12.5.  
XX  
OS Synthetic.  
XX  
DE Key Location/Qualifiers  
XX  
FH Region 1..114  
FT /label= VH\_NQ10/12.5  
FT Peptide 115..116  
FT /note= "Linker peptide"  
FT Region 117..223  
FT /label= Vkappa\_NQ10/12.5  
XX  
FN WO9303151-A1.  
XX  
PD 18-FEB-1993.  
XX  
PE 10-AUG-1992; 92WO-GB001483.  
XX  
PR 10-AUG-1991; 91GB-00017352.  
PR 11-JUN-1992; 92GB-00012419.  
XX  
PA (MED1-) MEDICAL RES COUNCIL.  
XX  
PI Embleton MJ, Gorochoy G, Jones PT, Winter GP;  
XX  
XX WPI; 1993-076508/09.  
DR N-PSDB; AAQ37460.  
XX  
PT Treatment of cell populations, partic. hybridomas - to link together  
PT copies of 2 or more non-contiguous DNA sequences to facilitate analysis.  
XX  
PS Disclosure; Fig 3; 72pp; English.  
XX  
CC The sequences given in AAR32840-43 show the mature heavy chain VH domains  
CC and the VK light chain genes of the antiphenylloxazolone hybridomas  
CC NQ2/12.4 and NQ10/12.5 which have been linked via a linker peptide by in-  
CC cell PCR. The cDNA encoding these peptides was synthesised using forward  
CC primers annealing to the Ck gene and the JH segment, followed by assembly  
CC with linker primers, VH back primers based on the VH3 leader sequence and  
CC a forward Ck primer nested in respect to the primer used for cDNA. The  
CC assembled product within the cells is then amplified with nested primers  
CC annealing to the 5' end of the VH gene and the 3' end of the Jk segment.  
CC In-cell PCR may be used to determine gene linkage analysis, particularly  
CC for the cloning of gene combinations that are polymorphic within a  
CC population of cells, such as the rearranged genes for Ig or TCR V  
CC regions. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 223 AA;  
XX



KM B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;  
KM T cell activation; inhibitor; graft versus host disease;  
KM transplant rejection; allograft rejection; autoimmune disease; allergy;  
KM therapy; human; bispecific tetraivalent antibody; BiTab;  
KM BiTab1G10-B7-24H6.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key  
FH Region  
FT Location/Qualifiers  
FT 1..120  
FT /note="VH region anti B7.2 MAb"  
FT 121..135  
FT /note="(G4S3) flexible linker"  
FT Region  
FT 136..248  
FT /note="VL region anti B7.2 MAB"  
FT Region  
FT 249..259  
FT /note="human IgG3 hinge region"  
FT 260..285  
FT /note="helix-turn-helix dimerization domain"  
FT Domain  
FT 286..305  
FT /note="human IgG3 hinge domain"  
FT Region  
FT 306..426  
FT /note="VH region anti B7.1 MAB"  
FT Peptide  
FT 427..441  
FT /note="(G4S3)flexible linker"  
FT Region  
FT 442..550  
FT /note="VL region anti B7.1 MAB"  
FT Peptide  
FT 551..556  
FT /note="hi66 tag"  
XX  
PN WO9658965-A2.  
XX  
PD 30-DEC-1998.  
XX  
PP 22-JUN-1998; 98WO-EP003791.  
XX  
PR 20-JUN-1997; 97EP-00870092.  
XX  
PA (INNO-) INNOGENETICS NV.  
PI Lorre K, Sablon E, Buyse M, Bosman A;  
XX  
XX WPI; 1999-105615/09.  
DR N-PSDB; AAX01652.  
XX  
PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat  
PT immune diseases including allograft rejection.  
XX  
PS Example 7.1; Fig 18; 182pp; English.  
XX  
XX This polypeptide comprises the bispecific tetraivalent antibody BiTab1G10-  
CC B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2  
CC anti B7.2 scFvs (tetraavalency). One single BiTab is a homodimer of 2  
CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv  
CC (bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a  
CC dimerization domain (see AAW90219), which drives the homodimerization of  
CC the molecule. DNA (see AAX01652) encoding the BiTab has been constructed  
CC to allow expression of the BiTab in transformed E. coli cells. The BiTab  
CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1  
CC and B7.2 that are expressed on the membrane of professional antigen-  
CC presenting cells, leading to the inhibition of antigen-specific T cell  
CC activation. The invention relates to such B7-binding molecules, methods  
CC for their production, and their use for treating or preventing diseases  
CC of the immune system, in particular graft rejection, graft versus host  
CC disease, allergy and autoimmune diseases (Claimed)  
XX  
SQ Sequence 556 AA;

Query Match 61.7%; Score 1001; DB 2; Length 556;  
Best Local Similarity 79.3%; Pred. No. 2e-63;

Matches 192; Conservative 20; Mismatches 26; Indels 4; Gaps 2;  
QY 1 MAEVLQSGGGGLVPGGSRRLSCAASGFTSSFGMHWVROAPEKLEWAVISSGSTI 60  
DB 309 LVQVQLQSGGGGLVPGGSRRLSCAASGFTSSFGMHWVROAPEKLEWAVISSSTLI 368  
QY 61 YYADTVKGRFTISRDNPCKLTFLQMTSLRSEDTVMYVYCARQ--YQAVYGGCTTVYVSSGG 118  
DB 369 YYADSVKGRFTISRDNPCKLTFLQMTSLRSEDTVMYVYCARQGWYPDVWGQGTTVYVSSGG 428  
QY 119 GSGGGGSGGGSDIELTQSPALMSASPGERVMTCSASSSVRYMN--WFOQSGTSPKR 176  
DB 429 GSGGGGSGGGSDIELTQSPSMAASVGDRTITCSVSRSSNLHWYQKSTSPRP 488  
QY 177 WIYDTSKLSSGVPAFSSGSGTSTSLTSSMEADAAVYVCOQSSNPLTFGAGTKLEL 236  
DB 489 WIYGTSLNASGVPSRFSGSGGTDTYTLTSSMQPEDAATVYVCOQSSVPLTFGQGTKEI 548  
QY 237 KR 238  
DB 549 KR 550  
RESULT 13  
AAE38657 standard; protein, 237 AA.  
ID AAE38657;  
AC AAE38657;  
XX  
XX 04-DEC-2003 (first entry)  
DT  
XX  
XX Mouse G1 single chain Fv-recombinant antibody.  
XX  
XX Major histocompatibility complex; MHC; HLA-restricted antigen; cancer;  
KM viral infection; autoimmune disease; gene therapy; cytostatic; virucide;  
KM immunomodulator; mouse.  
XX  
XX Mus sp.  
OS  
XX  
XX Key  
XX FH Location/Qualifiers  
XX FT 1..118  
XX FT /note="VH domain"  
XX FT 31..35  
XX FT /note="Complementarity determining region"  
XX FT 50..66  
XX FT /note="Complementarity determining region"  
XX FT 99..108  
XX FT /note="Complementarity determining region"  
XX FT 119..234  
XX FT /note="Peptide linker"  
XX FT 135..237  
XX FT /note="VL domain"  
XX FT 158..167  
XX FT /note="Complementarity determining region"  
XX FT 182..189  
XX FT /note="Complementarity determining region"  
XX FT 222..230  
XX FT /note="Complementarity determining region"  
XX PN WO2003068201-A2.  
XX  
XX 21-AUG-2003.  
XX  
XX 11-FEB-2003; 2003WO-IL000105.  
XX  
XX 13-FEB-2002; 2002US-00073301.  
XX  
XX (TECR ) TECHNION RES & DEV FOUND LTD.  
XX  
XX Reiter Y, Denkerberg G;  
XX  
XX WPI; 2003-689603/65.  
DR N-PSDB; AAD58607.



XX New isolated molecule comprising an antibody that binds with a human  
 PT major histocompatibility complex (MHC) class I being complexed with a HLA  
 PT -restricted antigen, useful for treating cancer, viral infection or  
 PT autoimmune disease.  
 XX  
 PS Claim 63, Fig 3a, 81pp, English.  
 XX  
 CC The invention relates to an isolated molecule comprising an antibody  
 CC specifically bindable with a binding affinity below 20 nanomolar to a  
 CC human major histocompatibility complex (MHC) class I being complexed with  
 CC a HLA-restricted antigen. The molecules, antibodies, and methods are  
 CC useful for treating cancer, viral infection and an autoimmune disease.  
 CC The invention is useful in gene therapy. The present sequence is mouse G1  
 CC single chain Fv-recombinant antibody  
 XX  
 SO Sequence 237 AA;  
 XX  
 Query Match 60.2%; Score 976.5; DB 7; Length 237;  
 Best Local Similarity 78.9%; Pred. No. 4.1e-62;  
 Matches 187; Conservative 18; Mismatches 27; Indels 5; Gaps 1;  
 QY 3 EVKLQSGGGGLVOPGSSRKLSCAASGFTSSFGMHWROAPEKLEWAVYISGSSITY 62  
 DB 1 QVTLQSGGGGLVOPGSSRKLSCAASGFTSSFGMHWROAPEKLEWAVYISGSSITY 60  
 QY 63 ADTVKGRFTISRDPKNTLFLQWTLRSDEPTVWYVCARD-----YGAHYGQGTITVVS 117  
 DB 61 PDSVKGRFTISRDPKNTLFLQWTLRSDEPTVWYVCARD-----YGAHYGQGTITVVS 120  
 QY 118 GGGSGGGGGGGSDIELTQSPAIMSASPERVTMTCSASSSVRYMWFQOKSGTSPKRW 177  
 DB 121 GGGSGGGGGGGSDIELTQSPAIMSASPERVTMTCSASSSVRYMWFQOKSGTSPRL 180  
 QY 178 IYDTSKLSSGVPARFSGSGSGTSLTISMEADATYYCQWSSNPLTFGAGT 234  
 DB 181 IYDTSNVAGVPRFSGSGSGTSLTINMEADATYYCQWSSNPLTFGAGT 237  
 RESULT 14  
 AAY44973  
 ID AAY44973 standard; protein; 268 AA.  
 AC AAY44973;  
 XX  
 XX 23-MAY-2000 (first entry)  
 DT  
 XX  
 DE Recombinant mouse anti-rotavirus antibody (Clone 22).  
 XX  
 XX Recombinant anti-rotavirus antibody; mouse; heavy chain variable region;  
 KM VH; light chain variable region; VL; PCANTAB 5E vector; treatment;  
 KM probiotic bacteria; antibacterial; antiviral; gastrointestinal tract;  
 KM immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.  
 XX  
 OS Synthetic.  
 OS Mus sp.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT 6..116  
 FT /label= Mouse\_Heavy\_chain\_variable\_region  
 FT 117..152  
 FT /label= Linker\_region  
 FT 153..250  
 FT /label= Mouse\_Light\_chain\_variable\_region  
 FT 254..266  
 FT /label= B\_tag\_domain  
 FT /note= "Enables immunodetection and immunospecificity  
 FT purification of the recombinant antibody"  
 XX  
 XX MO200006764-A1.  
 XX  
 XX 10-FEB-2000.  
 XX

PF 29-JUL-1999; 99WO-US017296.  
 XX  
 XX 30-JUL-1998; 98US-0094697P.  
 XX  
 PA (WISC) WISCONSIN ALUMNI RES FOUND.  
 PI Fahl WE, Letchworth GJ, Mueller GC, Savage AK, Loo D;  
 DR WPI; 2000-195315/17.  
 DR N-PSDB; AA250509.  
 XX  
 PT Composition for supplementing or replacing an immune response against  
 PT gastrointestinal pathogens in e.g. newborn infants, comprises probiotic  
 PT microorganisms expressing antibodies specific for the gastrointestinal  
 PT pathogens.  
 XX  
 XX  
 PS Disclosure; Fig 2; 48pp; English.  
 XX  
 CC The present sequence is the recombinant mouse anti-rotavirus antibody. It  
 CC comprises of mouse heavy chain (VH) and light chain (VL) variable regions  
 CC joined by a linker. The recombinant antibody encoding DNA is inserted  
 CC into PCANTAB 5E expression vector (clone 22). The vector is used to  
 CC transform probiotic bacteria like, Lactobacilli for expression and  
 CC secretion of recombinant anti-rotavirus antibodies. The antibodies have  
 CC antibacterial and antiviral activity. Antibody-expressing probiotic  
 CC bacteria can be administered for treatment of gastrointestinal (GI) tract  
 CC infections and to immunise neonates, humans or immunosuppressed/  
 CC immunodeficient adults acutely exposed to a bolus of GI pathogen  
 XX  
 SO Sequence 268 AA;  
 XX  
 Query Match 59.8%; Score 970.5; DB 3; Length 268;  
 Best Local Similarity 74.7%; Pred. No. 1.3e-61;  
 Matches 186; Conservative 24; Mismatches 30; Indels 9; Gaps 3;  
 QY 1 MAEVLQSGGGGLVOPGSSRKLSCAASGFTSSFGMHWROAPEKLEWAVYISGSSIT 60  
 DB 6 MAQVQLQSGGGGLVOPGSSRKLSCAASGFTSSFGMHWROAPEKLEWAVYISGSSIT 65  
 QY 61 YYADTVKGRFTISRDPKNTLFLQWTLRSDEPTVWYVCARDV-----AYWGQGTITV 113  
 DB 66 YYADTVKGRFTISRDPKNTLFLQWTLRSQDTAMVYCAR-WQNYPRYAMDVWGQGTITV 124  
 QY 114 VSSGGGGGGGGSDIELTQSPAIMSASPERVTMTCSASSSV-RYMWFFQOKSGT 172  
 DB 125 VSSGGGGGGGGSDIELTQSPAIMSASPERVTMTCSASSSV-RYMWFFQOKSGT 184  
 QY 173 SPKRWIYDTSKLSGVPARFSGSGSGTSLTISMEADATYYCQWSSNPLTFGAGT 232  
 DB 185 SPQFLVYSAKTLAEGVPSRFSGSGSGTQSLKINSIQPDPFGNYCQHYGSPRTFGAGT 244  
 QY 233 KLEIKRAAA 241  
 DB 245 KLEIKRAAA 253  
 RESULT 15  
 AAY44972  
 ID AAY44972 standard; protein; 268 AA.  
 AC AAY44972;  
 XX  
 XX 23-MAY-2000 (first entry)  
 DT  
 XX  
 DE Recombinant mouse anti-rotavirus antibody (Clone 11).  
 XX  
 XX Recombinant anti-rotavirus antibody; mouse; heavy chain variable region;  
 KM VH; light chain variable region; VL; PCANTAB 5E vector; treatment;  
 KM probiotic bacteria; antibacterial; antiviral; gastrointestinal tract;  
 KM immunise; neonate; immunosuppressed; immunodeficient; GI pathogen.  
 XX  
 OS Synthetic.  
 OS Mus sp.



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OM protein - protein search, using sw model

Run on: June 23, 2005, 05:52:38 ; Search time 1196 Seconds  
(without alignments)  
101.603 Million cell updates/sec

Title: US-09-403-882a-2

Perfect score: 1622  
Sequence: 1 MAEVLQESGGGVOPGSGSR.....VLLTITLILMLQMKPR 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/1/pubppa/US11A\_NEW\_PUB.pep.\*  
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22: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	959	59.1	291	US-10-406-830-10	Sequence 10, Appl
2	943.5	58.2	288	US-09-818-247-22	Sequence 22, Appl
3	940	58.0	244	US-10-879-994-16	Sequence 16, Appl
4	940	58.0	244	US-10-610-452-16	Sequence 16, Appl
5	928	57.2	499	US-10-805-177-111	Sequence 111, Appl
6	927	57.2	291	US-10-406-830-9	Sequence 9, Appl
7	926	57.1	287	US-10-406-830-5	Sequence 5, Appl
8	913	56.3	242	US-10-259-087A-20	Sequence 20, Appl
9	913	56.3	242	US-10-689-006-20	Sequence 20, Appl
10	907	55.9	353	US-09-503-958A-4	Sequence 4, Appl
11	906.5	55.9	237	US-09-880-748-2104	Sequence 2104, Ap

12	906.5	55.9	237	15	US-10-293-418-2104	Sequence 2104, Ap
13	903.5	55.7	237	10	US-09-880-748-2020	Sequence 2020, Ap
14	903.5	55.7	237	15	US-10-293-418-2020	Sequence 2020, Ap
15	900.5	55.5	237	10	US-09-880-748-2005	Sequence 2005, Ap
16	900.5	55.5	237	10	US-09-880-748-2114	Sequence 2114, Ap
17	900.5	55.5	237	15	US-10-293-418-2005	Sequence 2005, Ap
18	900.5	55.5	237	15	US-10-293-418-2114	Sequence 2114, Ap
19	899.5	55.5	237	10	US-09-880-748-2118	Sequence 2118, Ap
20	899.5	55.5	237	15	US-10-293-418-2118	Sequence 2118, Ap
21	899.5	55.5	639	17	US-10-792-498-16	Sequence 16, Appl
22	898.5	55.4	237	10	US-09-880-748-2115	Sequence 2115, Ap
23	898.5	55.4	237	15	US-10-293-418-2115	Sequence 2115, Ap
24	897.5	55.3	237	10	US-09-880-748-2027	Sequence 2027, Ap
25	897.5	55.3	237	10	US-09-880-748-2111	Sequence 2111, Ap
26	897.5	55.3	237	15	US-10-293-418-2027	Sequence 2027, Ap
27	897.5	55.3	237	15	US-10-293-418-2111	Sequence 2111, Ap
28	897.5	55.3	503	15	US-10-239-656-77	Sequence 77, Appl
29	897	55.3	256	15	US-10-239-656-61	Sequence 61, Appl
30	896.5	55.3	237	10	US-09-880-748-2003	Sequence 2003, Ap
31	896.5	55.3	237	10	US-09-880-748-2017	Sequence 2017, Ap
32	896.5	55.3	237	10	US-09-880-748-2019	Sequence 2019, Ap
33	896.5	55.3	237	10	US-09-880-748-2028	Sequence 2028, Ap
34	896.5	55.3	237	10	US-09-880-748-2110	Sequence 2110, Ap
35	896.5	55.3	237	15	US-10-293-418-2003	Sequence 2003, Ap
36	896.5	55.3	237	15	US-10-293-418-2017	Sequence 2017, Ap
37	896.5	55.3	237	15	US-10-293-418-2019	Sequence 2019, Ap
38	896.5	55.3	237	15	US-10-293-418-2028	Sequence 2028, Ap
39	896.5	55.3	237	15	US-10-293-418-2110	Sequence 2110, Ap
40	895.5	55.2	237	10	US-09-880-748-1906	Sequence 1906, Ap
41	895.5	55.2	237	15	US-10-293-418-1906	Sequence 1906, Ap
42	894.5	55.1	237	10	US-09-880-748-2040	Sequence 2040, Ap
43	894.5	55.1	237	15	US-10-293-418-2040	Sequence 2040, Ap
44	894	55.1	240	9	US-09-192-854-2	Sequence 2, Appl
45	894	55.1	240	9	US-09-968-561A-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-10-406-830-10  
; Sequence 10, Application US/10406830  
; Publication No. US20040071696A1  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, GREGORY P.  
; APPLICANT: HORAK, EVA M.  
; APPLICANT: WEINER, LOUIS M.  
; APPLICANT: JAMES, MARKS D.  
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
; FILE REFERENCE: 407T-000410US  
; CURRENT APPLICATION NUMBER: US/10/406, 830  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/370, 276  
; PRIOR FILING DATE: 2002-04-05  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-10

Query Match 59.1%; Score 959; DB 15; Length 291;

Best Local Similarity 70.1%; Pred. No. 2.2e-57;  
Matches 185; Conservative 31; Mismatches 38; Indels 10; Gaps 2;

QY 1 MAEVLQESGGGVOPGSGSRKSCASGTFPSFGHWRQAREKGLWAVYSSGSTI 60  
DB 21 MAQVQLQESGGGVOPGSRIRLSCASGTFSSYAMSWRQAPGKGLWVAISGSGST 80

```
QY 61 YYADTVKGFRTISRDNPKNTLFLQMTSLRSEDVTMYTCARD-----YGAVMGQGT 111
DB 81 YYADSVKGFRTISRDNPKNTLYLQNMNSLRAEDTALYYCARBEGYSNMNMWYFDLMGRGTL 140
QY 112 VVVSOGGSGGGGGGGGGSDIELTOSPAIMASPERVTMTCSASSV-RYMNWFOQGS 170
DB 141 VVVSOGGSGGGGGGGGGSEIVLTOSPSLSASVDRITTCRASOSISSTLMTYQKXP 200
QY 171 GTSPPKMIYDTSKLSGVPARFSGSGSTYSITSSMEADPAATYYCOOWSNPLTFGA 230
DB 201 GNAPKLLIYAASLSLQGVPSRFGSGSGTDFLTITISLQPDPAATYYCQYNSYPTFFGQ 260
QY 231 GTKLEIKRAAAEOKLISEEDLNGA 254
DB 261 GTKLEIKRAAAEOKLISEEDLNGA 284
```

## RESULT 2

```
US-09-818-247-22
/ Sequence 22, Application US/09818247
/ Patent No. US20020102657A1
/ GENERAL INFORMATION:
/ APPLICANT: Mostov, Keith E.
/ APPLICANT: Chapin, Steven J.
/ APPLICANT: Richman-Bienbat, Janice
/ TITLE OF INVENTION: The Regents of the University of California
/ TITLE OF INVENTION: Ligands directed to the No. US20020102657A1-Sstalk Region of p18r and Methods of Use Ther
/ FILE REFERENCE: 18062E-0009100S
/ CURRENT APPLICATION NUMBER: US/09/818,247
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: WO PCT/US01/09699
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: US 60/192,197
/ PRIOR FILING DATE: 2000-03-27
/ PRIOR APPLICATION NUMBER: US 60/192,198
/ PRIOR FILING DATE: 2000-03-27
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 288
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial
/ OTHER INFORMATION: Sequence: pelb/4AF/myc/SHIS
US-09-818-247-22
```

Query Match 58.2%; Score 943.5; DB 9; Length 288;

Best Local Similarity 69.3%; Pred. No. 2.4e-56;

Matches 181; Conservative 32; Mismatches 41; Indels 7; Gaps 2;

```
QY 1 MAEVLQESGGGLVOPGSRKLSGASGFTFSGFMHWVQAPKGLWVAAYISSGSSSTI 60
DB 21 MAQVLQVGGGLVOPGSLRLSCASGFTFSSSYAMSWRQAPKGLEWVAISSGSGST 80
QY 61 YYADTVKGFRTISRDNPKNTLFLQMTSLRSEDVTMYTCARD-----YGAVMGQGT 114
DB 81 YYADSVKGFRTISRDNPKNTLYLQNMNSLRAEDTALYYCARBEGYSNMNMWYFDLMGR 140
QY 115 SSGGGSGGGGGGGGGSDIELTOSPAIMASPERVTMTCSASSV-RYMNWFOQSGTS 173
DB 141 SSGGGSGGGGGGGGGSEIVLTOSPSLSASVDRITTCRASOSISSTLMTYQKXP 200
QY 174 PRMWYDTSKLSGVPARFSGSGSTYSITSSMEADPAATYYCOOWSNPLTFGAGTK 233
DB 201 PKLLIYKASSLSLQGVPSRFGSGSGTDFLTITISLQPDPAATYYCQYNSYPTFFGQTK 260
QY 234 LELKRAAAEOKLISEEDLNGA 254
DB 261 VDIKRAAAEOKLISEEDLNGA 281
```

## RESULT 3

```
US-10-879-994-16
/ Sequence 16, Application US/10879994
/ Publication No. US20050032175A1
/ GENERAL INFORMATION:
/ APPLICANT: Stahl, Neil
/ APPLICANT: Yancopoulos, George D.
/ APPLICANT: Yancopoulos, George D.
/ APPLICANT: Karrow, Margaret
/ TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METH
/ TITLE OF INVENTION: USE
/ FILE REFERENCE: REG 203E2
/ CURRENT APPLICATION NUMBER: US/10/879,994
/ PRIOR FILING DATE: 2004-06-29
/ PRIOR APPLICATION NUMBER: 10/610,452
/ PRIOR FILING DATE: 2003-06-30
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16
/ LENGTH: 244
/ TYPE: PRF
/ ORGANISM: mus musculus
US-10-879-994-16
```

Query Match 58.0%; Score 940; DB 17; Length 244;

Best Local Similarity 74.6%; Pred. No. 3.6e-56;

Matches 182; Conservative 22; Mismatches 32; Indels 8; Gaps 3;

```
QY 3 EYKLOESGGGLVOPGSRKLSGASGFTFSGFMHWVQAPKGLWVAAYISSGSSSTIY 62
DB 1 DVQLVESGGGLVOPGSRKLSGASGFTFSGFMHWVQAPKGLWVAAYISSGSSSTIY 60
QY 63 ADTVKGFRTISRDNPKNTLFLQMTSLRSEDVTMYTCARDYGA-----YMGQGTIVVSS 116
DB 61 ADTVKGFRTISRDNPKNTLFLQMTSLRSEDVTMYTCASSETARABAMYWGQGTIVVSS 120
QY 117 -GGGGSGGGGGGGGGSDIELTOSPAIMASPERVTMTCSASSV-RYMNWFOQSGTSP 174
DB 121 AGGGSGGGGGGGGGSDIOMTOSPASLSAVGETVITTCRASGNHNTLAWYQKQKSP 180
QY 175 KRWYDTSKLSGVPARFSGSGSTYSITSSMEADPAATYYCOOWSNPLTFGAGTK 234
DB 181 QLVVYNATLADGVPSRFGSGSGTQYSLKINSLOPDEFGSYCQFMSIPTFFGQTK 240
QY 235 ELKR 238
DB 241 ENKR 244
```

## RESULT 4

```
US-10-610-452-16
/ Sequence 16, Application US/10610452
/ Publication No. US20050074855A1
/ GENERAL INFORMATION:
/ APPLICANT: George D. Yancopoulos
/ APPLICANT: Neil Stahl
/ TITLE OF INVENTION: Cytokine-Specific Fusion Proteins and
/ TITLE OF INVENTION: Therapeutic and Diagnostic Methods For Use
/ FILE REFERENCE: REG 203E
/ CURRENT APPLICATION NUMBER: US/10/610,452
/ PRIOR FILING DATE: 2003-06-30
/ PRIOR APPLICATION NUMBER: 09/787,835
/ PRIOR FILING DATE: 2001-03-22
/ PRIOR APPLICATION NUMBER: PCT/US9/22045
/ PRIOR FILING DATE: 1999-04-19
/ PRIOR APPLICATION NUMBER: 09/313,942
/ PRIOR FILING DATE: 1999-04-19
/ PRIOR APPLICATION NUMBER: 60/101,858
/ PRIOR FILING DATE: 1999-09-25
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 16
/ LENGTH: 244
```

TYPE: PRT  
ORGANISM: homo sapiens  
US-10-610-452-16

Query Match 58.0%; Score 940; DB 17; Length 244;  
Best Local Similarity 74.6%; Pred. No. 3.6e-56;  
Matches 182; Conservative 22; Mismatches 32; Indels 8; Gaps 3;

QY 3 EVKLQESGGGLVOPGSGRKLSCAAGFTFSSFGMHVWROAPEKLEWAVYISGSSITTY 62  
DB 1 DVQLVSSGGGLVOPGSGRKLSCAAGFTFSSFGMHVWROAPEKLEWAVYISGSSITTY 60  
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTWYTCARDY-----YWGQGTIVVSS 116  
DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTWYTCARDY-----YWGQGTIVVSS 120  
QY 117 -GG 174  
DB 121 AGGG 180  
QY 175 KRWIYDTSKLSGVPARFSGSGSGTSLTSSMEADATYTCQOWSSNPLTFGAGTKL 234  
DB 181 QLLVYNAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFGSYICQLFWSLPMTFGGTKL 240  
QY 235 ELKR 238  
DB 241 ENKR 244

## RESULT 5

US-10-805-177-111  
Sequence 111, Application US/10805177  
Publication No. US2005008449A1  
GENERAL INFORMATION:  
APPLICANT: Landee, Gregory M.  
APPLICANT: Chen, Francine  
APPLICANT: Bezabeh, Binyam  
APPLICANT: Folz, Ian  
APPLICANT: Tse, Kam Fai  
APPLICANT: Jeffere, Michael  
APPLICANT: Meertl, Mehdi  
APPLICANT: Starling, Gary  
APPLICANT: Mezes, Peter  
APPLICANT: Khrantsov, Nikolai  
TITLE OF INVENTION: ANTIBODIES AGAINST T CELL IMMUNOGLOBULIN  
FILE REFERENCE: ABXCR.006A  
CURRENT FILING DATE: 2004-03-19  
PRIOR APPLICATION NUMBER: 60/456,652  
PRIOR FILING DATE: 2003-03-19  
NUMBER OF SEQ ID NOS: 141  
SOFTWARE: FaestSeq for windows Version 4.0  
SEQ ID NO 111  
LENGTH: 499  
TYPE: PRT  
ORGANISM: Homo Sapiens  
US-10-805-177-111

Query Match 57.2%; Score 928; DB 17; Length 499;  
Best Local Similarity 52.2%; Pred. No. 5e-55;  
Matches 184; Conservative 16; Mismatches 26; Indels 136; Gaps 3;

QY 2 AEVKLOESGGGLVOPGSGRKLSCAAGFTFSSFGMHVWROAPEKLEWAVYISGSSITTY 61  
DB 128 SQVLVESGGGVOPGSLRLSCAAGFTFSSFGMHVWROAPEKLEWAVYISGSSITTY 187  
QY 62 YADTVKGRFTISRDNPKNTLFLQMTSLRSEDTWYTCARDY-----GAYWQGTIV 112  
DB 188 YADSVKGRFTISRDNPKNTLFLQMTSLRSEDTWYTCARDY-----GAYWQGTIV 247  
QY 113 TVSSGGGG----- 121

DB 248 TVSSGGGGSDIKLQSGAELARPASVKNKCTSGTTPRTYTMWVKORPGGLEWIGYI 307  
QY 122 ----- 121

DB 308 NPERGYTNVQKFKDAITLTDKSSSTAYMQLSLTSEDSAVYTCARYDDHCLDYWGQ 367  
QY 122 -----GGGGGGGG--SDIELTOSPAIMASPGERVMTTCASSSVRYMNV 165  
DB 368 GTLLTVSSVEGGSGGGSGGGVDDIQLTOSPAIMASPGERVMTTCASSSVRYMNV 427  
QY 166 FQKSGTSEKRWIYDTSKLSGVPARFSGSGSTSLTSSMEADATYTCQOWSSNP 225  
DB 428 YQKSGTSEKRWIYDTSKLSGVPARFSGSGSTSLTSSMEADATYTCQOWSSNP 487  
QY 226 LTFGAGTKLEK 237  
DB 488 LTFGAGTKLEK 499

## RESULT 6

US-10-406-830-9  
Sequence 9, Application US/10406830  
Publication No. US20040071696A1  
GENERAL INFORMATION:  
APPLICANT: ADAMS, GREGORY P.  
APPLICANT: HORAK, EVA M.  
APPLICANT: WEINER, LOUIS M.  
APPLICANT: JAMES, MARKS D.  
TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE  
FILE REFERENCE: 407T-000410US  
CURRENT FILING DATE: 2003-04-04  
PRIOR APPLICATION NUMBER: US 60/370,276  
PRIOR FILING DATE: 2002-04-05  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 9  
LENGTH: 291  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic antibody.  
US-10-406-830-9

Query Match 57.2%; Score 927; DB 15; Length 291;  
Best Local Similarity 67.4%; Pred. No. 3.3e-55;  
Matches 178; Conservative 36; Mismatches 40; Indels 10; Gaps 2;

QY 1 MAEVLQESGGGLVOPGSGRKLSCAAGFTFSSFGMHVWROAPEKLEWAVYISGSSITTY 60  
DB 21 MAOVLLQGGGLVOPGSLRLSCAAGFTFSSFGMHVWROAPEKLEWAVYISGSSITTY 80  
QY 61 YVADTVKGRFTISRDNPKNTLFLQMTSLRSEDTWYTCARDY-----YGAWQGTIV 111  
DB 81 YVADSVKGRFTISRDNPKNTLFLQMTSLRSEDTWYTCARDY-----YGAWQGTIV 140  
QY 112 TVSSGG 170  
DB 141 TVSSGG 200  
QY 171 GTSPEKWIYDTSKLSGVPARFSGSGSTSLTSSMEADATYTCQOWSSNPLTFGA 230  
DB 201 GKAPPELLITAASLQGVPSRFSGSGSTFETLITSLQDPDPAITTYGQYVYVYPTFGF 260  
QY 231 GTYELKRAAEEQKLISEEDLNGA 254  
DB 261 GTYELKRAAEEQKLISEEDLNGA 284

## RESULT 7

US-10-406-830-5  
Sequence 5, Application US/10406830

```
Publication No. US20040071696A1
GENERAL INFORMATION:
APPLICANT: ADAMS, GREGORY P.
APPLICANT: HORAK, EVA M.
APPLICANT: WEINER, LOUIS M.
APPLICANT: JAMES, MARKS D.
TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
FILE REFERENCE: 407T-000410US
CURRENT APPLICATION NUMBER: US/10/406,830
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/370,276
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 287
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic antibody.
US-10-406-830-5
```

```
Query Match 57.1%; Score 926; DB 15; Length 287;
Best Local Similarity 69.6%; Pred. No. 3.8e-55;
Matches 181; Conservative 32; Mismatches 41; Indels 6; Gaps 3;
```

```
QY 1 MAEVKLQSSGGGLVOPGSGSRKLSCAASGFTFSSFGMHVROAPEKGLWAVAYISSGSSSTI 60
DB 21 MAQVQLQSSGGGLVOPGSGSRKLSCAASGFTFSDYIHWKRAQKGLWAVAYISSGSSSTI 80
QY 61 YYADTVKGRFTISRDPKNTLFLQWTSLSRSDTVMYCAR--DYGA--YMGQGTIVYSS 116
DB 81 YYAAVKQKFTISRDPKNTLFLQWTSLSRSDTVMYCAR--DYGA--YMGQGTIVYSS 140
QY 116 SGGSGSGSGSGSGSDIELTQSPAIMSASPERVMTCSASSV-RYNNMFQOKSGTSPR 174
DB 141 SGGSGSGSGSGSGSDIQMTQSPSTLSASLSDRVITTRASQSIGSWLAWYQOKRGPAP 200
QY 175 KMWYDTSKLSGVPARFSGSGSTSYSLTISMEADATYYCOQWSSNPLTFGAGTKLEL 234
DB 201 KLIYKASLTLSGVPARFSGSGSTSYSLTISMEADATYYCOQWSSNPLTFGAGTKLEL 260
QY 235 ELKRAAAEQKLISEEDLNCA 254
DB 261 ELKRAAAEQKLISEEDLNCA 280
```

## RESULT 8

```
US-10-259-087A-20
Sequence 20, Application US/10259087A
Publication No. US20030130190A1
GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Hallahan, Dennis E
APPLICANT: Qu, Shihlan
TITLE OF INVENTION: IN VIVO PANNING FOR LIGANDS TO RADIATION-INDUCED MOLECULES
FILE REFERENCE: 1242/47/2
CURRENT APPLICATION NUMBER: US/10/259,087A
CURRENT FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/328123
PRIOR FILING DATE: 2001-10-03
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 242
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial antibody ligand number 2
US-10-259-087A-20
```

```
Query Match 56.3%; Score 913; DB 14; Length 242;
```

```
Best Local Similarity 71.1%; Pred. No. 2.4e-54;
Matches 172; Conservative 30; Mismatches 36; Indels 4; Gaps 2;
QY 1 MAEVKLQSSGGGLVOPGSGSRKLSCAASGFTFSSFGMHVROAPEKGLWAVAYISSGSSSTI 60
DB 1 MAQVQLQSSGGGLVOPGSGSRKLSCAASGFTFSDYIHWKRAQKGLWAVAYISSGSSSTI 80
QY 61 YYADTVKGRFTISRDPKNTLFLQWTSLSRSDTVMYCAR--DYGA--YMGQGTIVYSS 116
DB 61 KYNEFKKKAALTSRDPKNTLFLQWTSLSRSDTVMYCAR--DYGA--YMGQGTIVYSS 120
QY 117 GGGSGSGSGSGSDIELTQSPAIMSASPERVMTCSASSVRYNNMFQOKSGTSPR 176
DB 121 GGGSGSGSGSGSDIELTQSPAIMSASPERVMTCSASSVRYNNMFQOKSGTSPR 180
QY 177 KMWYDTSKLSGVPARFSGSGSTSYSLTISMEADATYYCOQWSSNPLTFGAGTKLEL 236
DB 181 KLIYKASLTLSGVPARFSGSGSTSYSLTISMEADATYYCOQWSSNPLTFGAGTKLEL 240
QY 237 KR 238
DB 241 KR 242
```

## RESULT 9

```
US-10-689-006-20
Sequence 20, Application US/10689006
Publication No. US20040191249A1
GENERAL INFORMATION:
APPLICANT: Vanderbilt University
APPLICANT: Hallahan, Dennis E
APPLICANT: Wernau, Raymond
TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
FILE REFERENCE: 1242/72
CURRENT APPLICATION NUMBER: US/10/689,006
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: US 09/914,605
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 10/259,087
PRIOR FILING DATE: 2002-09-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 242
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Artificial antibody ligand number 2
US-10-689-006-20
```

```
Query Match 56.3%; Score 913; DB 16; Length 242;
Best Local Similarity 71.1%; Pred. No. 2.4e-54;
Matches 172; Conservative 30; Mismatches 36; Indels 4; Gaps 2;
```

```
QY 1 MAEVKLQSSGGGLVOPGSGSRKLSCAASGFTFSSFGMHVROAPEKGLWAVAYISSGSSSTI 60
DB 1 MAQVQLQSSGGGLVOPGSGSRKLSCAASGFTFSDYIHWKRAQKGLWAVAYISSGSSSTI 80
QY 61 YYADTVKGRFTISRDPKNTLFLQWTSLSRSDTVMYCAR--DYGA--YMGQGTIVYSS 116
DB 61 KYNEFKKKAALTSRDPKNTLFLQWTSLSRSDTVMYCAR--DYGA--YMGQGTIVYSS 120
QY 117 GGGSGSGSGSGSDIELTQSPAIMSASPERVMTCSASSVRYNNMFQOKSGTSPR 176
DB 121 GGGSGSGSGSGSDIELTQSPAIMSASPERVMTCSASSVRYNNMFQOKSGTSPR 180
QY 177 KMWYDTSKLSGVPARFSGSGSTSYSLTISMEADATYYCOQWSSNPLTFGAGTKLEL 236
DB 181 KLIYKASLTLSGVPARFSGSGSTSYSLTISMEADATYYCOQWSSNPLTFGAGTKLEL 240
QY 237 KR 238
DB 241 KR 242
```









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OM protein - protein search, using sw model

Run on: June 23, 2005, 05:50:29 ; Search time 25 Seconds  
(without alignments) 943.564 Million cell updates/sec

Title: US-09-403-882a-2

Perfect score: 1622  
Sequence: 1 MAEVKLQESGGIVOPGSGSR.....VLLTIIILITLMQKPR 316

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents RA:\*

- 1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/1aa/PCUS\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/1aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1319	81.3	255	3 US-09-553-498-8	Sequence 8, Appl1
2	1319	81.3	255	4 US-09-518-869-8	Sequence 8, Appl1
3	1199	73.9	236	2 US-08-190-199A-65	Sequence 65, Appl1
4	1185	73.1	240	2 US-08-956-047-25	Sequence 25, Appl1
5	1102.5	68.0	223	2 US-08-190-199A-63	Sequence 63, Appl1
6	964.5	59.5	284	3 US-08-564-164A-2	Sequence 2, Appl1
7	943.5	58.2	225	2 US-08-190-199A-61	Sequence 61, Appl1
8	919	56.7	553	2 US-08-661-052-16	Sequence 16, Appl1
9	919	56.7	553	3 US-09-188-082-16	Sequence 16, Appl1
10	919	56.7	553	3 US-09-364-088-16	Sequence 16, Appl1
11	919	56.7	553	3 US-09-102-716-16	Sequence 16, Appl1
12	907	55.9	353	4 US-09-203-858A-4	Sequence 4, Appl1
13	900.5	55.5	281	3 US-09-423-439-44	Sequence 44, Appl1
14	897.5	55.1	240	4 US-09-138-091A-76	Sequence 76, Appl1
15	894	55.1	240	4 US-09-192-854-2	Sequence 2, Appl1
16	890.5	54.9	245	3 US-08-918-148-75	Sequence 75, Appl1
17	890.5	54.9	245	3 US-08-918-148-78	Sequence 78, Appl1
18	890.5	54.9	245	4 US-09-138-091A-73	Sequence 73, Appl1
19	881.5	54.3	245	3 US-08-918-148-76	Sequence 76, Appl1
20	881.5	54.3	245	4 US-09-138-091A-74	Sequence 74, Appl1
21	877	54.1	270	2 US-08-652-507-2	Sequence 2, Appl1
22	876.5	54.0	238	4 US-09-798-689-21	Sequence 21, Appl1
23	873.5	53.9	301	2 US-08-661-052-14	Sequence 14, Appl1
24	873.5	53.9	301	3 US-09-188-082-14	Sequence 14, Appl1
25	873.5	53.9	301	3 US-09-364-088-14	Sequence 14, Appl1
26	873.5	53.9	301	3 US-09-102-716-14	Sequence 14, Appl1
27	864	53.3	258	4 US-09-526-738A-4	Sequence 4, Appl1

28	861	53.1	239	3 US-08-279-772A-8	Sequence 8, Appl1
29	861	53.1	239	3 US-08-902-486-11	Sequence 11, Appl1
30	861	53.1	282	2 US-08-860-174A-10	Sequence 10, Appl1
31	859	53.0	495	4 US-09-948-004-18	Sequence 18, Appl1
32	858.5	52.9	284	3 US-09-184-658-40	Sequence 40, Appl1
33	858.5	52.9	284	4 US-09-504-262D-40	Sequence 40, Appl1
34	855	52.7	244	4 US-08-918-148-77	Sequence 77, Appl1
35	855	52.7	244	4 US-09-138-091A-75	Sequence 75, Appl1
36	855	52.7	256	4 US-09-526-738A-2	Sequence 2, Appl1
37	853.5	52.6	242	2 US-08-553-497A-26	Sequence 26, Appl1
38	852	52.5	599	1 US-08-463-163-3	Sequence 3, Appl1
39	851	52.5	246	1 US-08-469-486-57	Sequence 57, Appl1
40	851	52.5	246	2 US-08-469-658-57	Sequence 57, Appl1
41	850	52.4	666	3 US-09-423-439-51	Sequence 51, Appl1
42	847	52.2	222	2 US-08-190-199A-67	Sequence 67, Appl1
43	840.5	51.8	241	4 US-09-581-345-5	Sequence 5, Appl1
44	840.5	51.8	244	4 US-08-553-497A-20	Sequence 20, Appl1
45	838.5	51.7	242	2 US-08-553-497A-28	Sequence 28, Appl1

## ALIGNMENTS

RESULT 1  
US-09-553-498-8  
; Sequence 8, Application US/09553498  
; Patent No. 6309861  
; GENERAL INFORMATION:  
; APPLICANT: Ambrosius, Dorothee  
; APPLICANT: Rudolph, Rainer  
; APPLICANT: Schaeffner, Joerg  
; APPLICANT: Schwarz, Elisabeth  
; TITLE OF INVENTION: Process for the production of naturally folded and secreted protei  
; FILE REFERENCE: Case 20379  
; CURRENT APPLICATION NUMBER: US/09/553,498  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: EP99107412.1  
; PRIOR FILING DATE: 1999-04-26  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 8  
; LENGTH: 255  
; TYPE: PRT  
; ORGANISM: E. coli  
; US-09-553-498-8

Query Match 81.3%; Score 1319; DB 3; Length 255;  
Best Local Similarity 99.2%; Pred. No. 8.6e-91;  
Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVKLQESGGIVOPGSGSRKLSCAASGFTFSGFMHWROAPEKLEWVAIYSSGSTI 60  
DB 1 MAEVKLQESGGIVOPGSGSRKLSCAASGFTFSGFMHWROAPEKLEWVAIYSSGSTI 60  
QY 61 YYADTYKGRFTISRDPKNTLFLQMTSLRSEDTWYTCARDYCAVGGCTTVVSSGGG 120  
DB 61 YYADTYKGRFTISRDPKNTLFLQMTSLRSEDTWYTCARDYCAVGGCTTVVSSGGG 120  
QY 121 SGGGSGGGGSDIELTQSPALMSASPERVTWTCASSSVRVNMWFOQSGTSPKRWYD 180  
DB 121 SGGGSGGGGSDIELTQSPALMSASPERVTWTCASSSVRVNMWFOQSGTSPKRWYD 180  
QY 181 TSKLSSGVAFRFSGSGSTYSITLTISSMEADATYTCQWSSNPITFGAGTLEIKRAA 240  
DB 181 TSKLSSGVAFRFSGSGSTYSITLTISSMEADATYTCQWSSNPITFGAGTLEIKRAA 240  
QY 241 AEQKLISEEDLNGA 254  
DB 241 AEQKLISEEDLNGA 254

RESULT 2  
US-09-618-869-8  
; Sequence 8, Application US/09618869

Patent No. 6455279  
GENERAL INFORMATION:  
APPLICANT: Ambrosius, Dorthée  
APPLICANT: Rudolph, Rainer  
APPLICANT: Schaeffner, Joerg  
APPLICANT: Schwarz, Elisabeth  
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND  
SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR  
TITLE OF INVENTION: CHAPERONES  
FILE REFERENCE: 20381  
CURRENT APPLICATION NUMBER: US/09/618,869  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: EP9911481.5  
PRIOR FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 8  
LENGTH: 255  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-618-869-8

Query Match 81.3%; Score 1319; DB 4; Length 255;  
Best Local Similarity 99.2%; Pred. No. 8, 6e-91;  
Matches 252; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAEVKIQESGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLGVAVYISSGSSSTI 60  
DB 1 MAEVKIQESGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLGVAVYISSGSSSTI 60  
QY 61 YVADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTWYVCARDYGAVWCGGTTVTYSSGGGSG 120  
DB 61 YVADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTWYVCARDYGAVWCGGTTVTYSSGGGSG 120  
QY 121 SGGSGSGGGGSDIELTOSPAIMASPERVTWTCASSSSVRYNMWFOOKSGTSPKRIYD 180  
DB 121 SGGSGSGGGGSDIELTOSPAIMASPERVTWTCASSSSVRYNMWFOOKSGTSPKRIYD 180  
QY 181 TSKLSGVPARFSGSGGTSYSTLTSSMEADATYYCCQMSNPLTFGAGTKLELRAA 240  
DB 181 TSKLSGVPARFSGSGGTSYSTLTSSMEADATYYCCQMSNPLTFGAGTKLELRAA 240  
QY 241 AEOKLISEEDLNGA 254  
DB 241 AEOKLISEEDLNGA 254

RESULT 3  
US-08-190-199A-65  
Sequence 65, Application US/08190199A  
Patent No. 5830663

GENERAL INFORMATION:  
APPLICANT: EMBLETON, Michael J.  
APPLICANT: GOROCIOV, Guy  
APPLICANT: JONES, Peter T.  
APPLICANT: WINTER, Gregory P.  
TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILSBURY MADISON & SUTRO, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3918  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/190,199A  
FILING DATE: 13-JUL-1994

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB92/01483  
FILING DATE: 10-AUG-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9212419.7  
FILING DATE: 11-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9117352.6  
FILING DATE: 10-AUG-1991  
INFORMATION FOR SEQ ID NO: 65:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 236 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-190-199A-65

Query Match 73.9%; Score 1199; DB 2; Length 236;  
Best Local Similarity 96.2%; Pred. No. 6, 8e-82;  
Matches 227; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 EYKIQESGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLGVAVYISSGSSSTIY 62  
DB 1 DVQLVESGGGLVOPGSGSRKLSCAASGFTFSSFGMHVWROAPEKGLGVAVYISSGSSSTIY 60  
QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTWYVCARDYGAVWCGGTTVTYSSGGGSG 122  
DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDVTWYVCARDYGAVWCGGTTVTYSSAGGSG 120  
QY 123 GGGSGGGGSDIELTOSPAIMASPERVTWTCASSSSVRYNMWFOOKSGTSPKRIYDTS 182  
DB 121 GGGSGGGGSDIELTOSPAIMASPERVTWTCASSSSVRYNMWFOOKSGTSPKRIYDTS 180  
QY 183 KLSGVPARFSGSGGTSYSTLTSSMEADATYYCCQMSNPLTFGAGTKLELR 238  
DB 181 KLSGVPARFSGSGGTSYSTLTSSMEADATYYCCQMSNPLTFGAGTKLELR 236

RESULT 4  
US-08-956-047-25  
Sequence 25, Application US/08956047  
Patent No. 5882924

GENERAL INFORMATION:  
APPLICANT: Fritz, Hans-Joachim  
APPLICANT: Hennecke, Frank  
APPLICANT: Kolmar, Harald  
TITLE OF INVENTION: Genetic Selection, by Means of Signal  
TITLE OF INVENTION: Transduction in Microorganisms, of Proteins which are  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegans, Henderson, Farabow, Garrett & Dunner  
STREET: 1300 I Street, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,047  
FILING DATE: 22-OCT-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/257,669  
FILING DATE: 08-JUN-1994  
APPLICATION NUMBER: DE P 43 19 296.3  
FILING DATE: 10-JUN-1993  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Pohlman, Sandra M.  
 REGISTRATION NUMBER: P39, 691  
 REFERENCE/DOCKET NUMBER: 05552.1368-00000  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-408-4000  
 TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 240 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-956-047-25

Query Match 73.1%; Score 1185; DB 2; Length 240;  
 Best Local Similarity 95.7%; Pred. No. 7, 6e-81;  
 Matches 225; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 VKLQESGGGLVQPGSGSKLSCAASGFTFSFGMHVROAPEKGLQWVAIYSSGSSSTIYYA 63  
 DB 6 VQVLELGGFVQPGSGSKLSCAASGFTFSFGMHVROAPEKGLQWVAIYSSGSSSTIYYA 65  
 QY 64 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTWYVYCARVGYAWGQGLTVTVSSGGGSGG 123  
 DB 66 DTVKGRFTISRDNPKNTLFLQMTSLRSEDTWYVYCARVGYAWGQGLTVTVSSGGGSGG 125  
 QY 124 GSGGGGSDIELTOSPAIMSASPGERVMTCSASSSVRYMNFQOKSGTSPKRWIYDTS 183  
 DB 126 GSGGGGSDIQLTOSPAIMSASPGERVMTCSASSSVRYMNFQOKSGTSPKRWIYDTS 185  
 QY 184 LSSGVPAFSGSGSGTSTSLTSSMEADAAATYCCQMSNPLTFGAGTKLELR 238  
 DB 186 LSSGVPAFSGSGSGTSTSLTSSMEADAAATYCCQMSNPLTFGAGTKLELR 240

RESULT 5  
 US-08-190-199A-63  
 Sequence 63, Application US/08190199A  
 Patent No. 5830663

GENERAL INFORMATION:  
 APPLICANT: EMBLETON, Michael J.  
 APPLICANT: GOROCIOV, Guy  
 APPLICANT: JONES, Peter T.  
 APPLICANT: WINTER, Gregory P.  
 TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS  
 NUMBER OF SEQUENCES: 70  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Microsoft Word  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/190,199A  
 FILING DATE: 13-JUL-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB92/01483  
 FILING DATE: 10-AUG-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9212419.7  
 FILING DATE: 11-JUN-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: GB 9117352.6  
 FILING DATE: 10-AUG-1991  
 INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 223 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-190-199A-63

Query Match 68.0%; Score 1102.5; DB 2; Length 223;  
 Best Local Similarity 90.3%; Pred. No. 9, 8e-75;  
 Matches 213; Conservative 4; Mismatches 6; Indels 13; Gaps 1;

QY 3 EYKLQESGGGLVQPGSGSKLSCAASGFTFSFGMHVROAPEKGLQWVAIYSSGSSSTIYY 62  
 DB 1 DVQVLESGGGGLVQPGSGSKLSCAASGFTFSFGMHVROAPEKGLQWVAIYSSGSSSTIYY 60  
 QY 63 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTWYVYCARVGYAWGQGLTVTVSSGGGSGG 122  
 DB 61 ADTVKGRFTISRDNPKNTLFLQMTSLRSEDTWYVYCARVGYAWGQGLTVTVSSGGGSGG 114  
 QY 123 GSGGGGSDIELTOSPAIMSASPGERVMTCSASSSVRYMNFQOKSGTSPKRWIYDTS 182  
 DB 115 -----ASQIVLTQSPAIMSASPGERVMTCSASSSVRYMNFQOKSGTSPKRWIYDTS 167  
 QY 183 KLSGVPAFSGSGSGTSTSLTSSMEADAAATYCCQMSNPLTFGAGTKLELR 238  
 DB 168 KLSGVPAFSGSGSGTSTSLTSSMEADAAATYCCQMSNPLTFGAGTKLELR 223

RESULT 6  
 US-08-564-164A-2  
 Sequence 2, Application US/08564164A  
 Patent No. 6159947

GENERAL INFORMATION:  
 APPLICANT: Schweighofer, Fabien  
 APPLICANT: Tocque, Bruno  
 TITLE OF INVENTION: Intracellular Binding Proteins and Use  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Rhone-Poulenc Rorer Inc.  
 STREET: 500 Arcola Road, 3043  
 CITY: Collegeville  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19426-0107  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/564,164A  
 FILING DATE: 28-DEC-1995  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/FR94/00714  
 FILING DATE: 15-JUN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: FR 93/07241  
 FILING DATE: 16-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Savitzky, Martin F.  
 REGISTRATION NUMBER: 29,699  
 REFERENCE/DOCKET INFORMATION:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610)454-3816  
 TELEFAX: (610)454-3808  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 284 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-564-164A-2

Query Match	59.5%;	Score 964.5;	DB 3;	Length 284;
Best Local Similarity	72.2%;	Pred. No. 2.5e-64;		
Matches 187;	Conservative 24;	Mismatches 41;	Indels 7;	Gaps 2;

[illegible]

## RESULT 7

US-08-190-199A-61  
; Sequence 61, Application US/08190199A

GENERAL INFORMATION:  
APPLICANT: EMBLETON, Michael J.  
APPLICANT: GOROCHOV, Guy  
APPLICANT: JONES, Peter T.  
APPLICANT: WINTER, Gregory P.  
TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PILSBURY MADISON & SUTRO, L.L.P.  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: D.C.

Query Match	58.2%;	Score 943.5;	DB 2;	Length 235;
Best Local Similarity	75.0%;	Pred. No. 7.2e-63;		

Matches 177; Conservative 26; Mismatches 32; Indels 1; Gaps 1,

QY 3 EYVLEDEGGGGLVQPPGSGRRKSCAASGPFSSFGHAWRQAPKEKLEWVAAYSSGSSSTYY 62

Db 1 QVQLEBSGEGVLVAPBSQSLSTICTWYSGBSLTISGVHWARPQPKGLBNGIYIMAGST-NY 59

QY 63 ADYVKGKPTISHDNKNTLFLQMTSLRSEDTVMYVYCARDYGAVMGGSTTVVSSGGGGSG 122

Db 60 NSALMSRLSLSDKNSKQVFLKMSLSLQTTDPTAMTYCARDRGAYVGGGLVTVSAGGGGGG 119

QY 123 GGGSGGGGGDIEILQSPAINGASPEERYVTMCSSSSYRYNMVFOQSGTSPKMYIDTS 182

Db 120 GGGSGGGGGQIYLITQSPAIMSASPEQKATMTCSSASSSYVHWVQOKSGTSPKMYIDTS 179

QY 183 KLSGVPAPRFSGSGSGTYSYLTLSMEADAATYYCOOMSNPLTFGAGTGLIELKR 238

Db 180 KLSGVPAPRFSGSGGATYSYLTLSMEADAATYYCOOMSNPLTFGAGTGLIELKR 235

## RESULT 8

US-08-661-052-16  
; Sequence 16, Application US/08661052

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1  GENERAL INFORMATION:
2  APPLICANT:  Yashwant M. Deo
3  APPLICANT:  Joel Goldstein
4  APPLICANT:  Robert Graziano
5  APPLICANT:  Chazian Somaasandaram
6  TITLE OF INVENTION:  THERAPEUTIC COMPOUNDS COMBRISE
7  TITLE OF INVENTION:  OF ANTI-FC RECEPTOR ANTIBODIES
8  NUMBER OF SEQUENCES:  16
9  CORRESPONDENCE ADDRESS:
10 ADDRESSER:  LAHIVE & COCKFIELD
11 STREET:  60 State Street, Suite 510
12 City:  Boston
13 STATE:  Massachusetts
14 COUNTRY:  USA
15 ZIP:  02109-1875
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE:  Floppy disk
18 COMPUTER:  IBM PC compatible
19 OPERATING SYSTEM:  PC-DOS/MS-DOS
20 SOFTWARE:  PatentIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER:  US/08/661,052
23 FILING DATE:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:  US 08/484,172
26 FILING DATE:  07-JUNE-1995
27 ATTORNEY/AGENT INFORMATION:
28 NAME:  Arnold, Beth E.
29 REGISTRATION NUMBER:  35,430
30 REFERENCE/DOCKET NUMBER:  MXI-043CP
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE:  (617)227-7400
33 TELEFAX:  (617)227-5941
34 INFORMATION FOR SEQ ID NO:  16:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH:  553 amino acids
37 type:  amino acid
38 TOPOLOGY:  linear
39 MOLECULE TYPE:  protein
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Query Match	56.7%	Score	919;	DB 2;	Length	553;			
Similarity	67.5%	Pred. No.	1.3e-60;						
Best Local									
Matches	183;	Conservative	22;	Mismatches	48;	Indels	18;	Gaps	2

[illegible]

Db 336 YAKFGKATFTTDTSSNTAYLQLSLTSEDDAAYVYCNMGFTPTGYPYFDYMGSGTITTVS 395

QY 116 SGGGGSGGGSGGGGGDIELTQSPAIMSAPGERVTMTCSASSVRYNMFQOKSGTSPK 175

Db 396 SGGGGSGGGSGGGGSENVLTQSPAIMSAPBEXTTITCSASSSVYHNMQKRGTSIPK 455

QY 176 RWIYDTSKLSSGVPARFSSGSGGTSTSLTSSMEADATATYCOQMSNPULTFGAGTKLE 235

Db 456 LWTYSTNLASGVPARFSSGSGGTSTSLTSSMEADATATYCOQRSYPLTFAGTKLE 515

QY 236 LKR-----AAAEQKLISEEDLNGA 254

Db 516 LKRAAGSSGGGSDIAAEQKLISEEDLNGA 546

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1      RESULT 9
2      US-09-188-082-16
3      Sequence 16, Application US/09188082
4      Patent No. 6270765
5      GENERAL INFORMATION:
6      APPLICANT: Yashwant M. Deo
7      APPLICANT: Joel Goldstein
8      APPLICANT: Robert Graziano
9      APPLICANT: Chezian Somaasandaram
10     TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
11     TITLE OF INVENTION: OF ANTI-PC RECEPTOR ANTIBODIES
12     NUMBER OF SEQUENCES: 16
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: LAHIVE & COCKFIELD
15     STREET: 60 State Street, Suite 510
16     CITY: Boston
17     STATE: Massachusetts
18     COUNTRY: USA
19     ZIP: 02109-1875
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: PatentIn Release #1.0, Version #1.25
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/09/188,082
27     FILING DATE:
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: 08/661,052
30     FILING DATE:
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Arnold, Beth E.
33     REGISTRATION NUMBER: 35,430
34     REFERENCE/DOCKET NUMBER: MX1-043CP
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: (617)227-7400
37     TELEFAX: (617)227-5941
38     INFORMATION FOR SEQ ID NO: 16:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 553 amino acids
41     TYPE: amino acid
42     TOPOLOGY: linear
43     MOLECULE TYPE: protein
44     US-09-188-082-16

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[illegible][illegible]

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1      RESULT 10
2      US-09-364-088-16
3      Sequence 16, Application US/09364088
4      Patent No. 6365161
5      GENERAL INFORMATION:
6      APPLICANT: Yashwant M. Deo, et al.
7      TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
8      TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
9      NUMBER OF SEQUENCES: 16
10     CORRESPONDENCE ADDRESS:
11     ADDRESSEE: LAHIVE & COCKFIELD, LLP
12     STREET: 28 State Street, 24th Floor
13     CITY: Boston
14     STATE: Massachusetts
15     COUNTRY: USA
16     ZIP: 02109
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: Patentln Release #1.0, Version #1.25
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/09/364,088
24     FILING DATE:
25     PRIOR APPLICATION DATA:
26     APPLICATION NUMBER: US 09/188,082
27     FILING DATE: 07-JUNE-1996
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: US 08/484,172
30     FILING DATE: 07-JUNE-1995
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Remillard, Jane E.
33     REGISTRATION NUMBER: 38,872
34     REFERENCE/DOCKET NUMBER: MXI-043CP2
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: (617)227-7400
37     TELEFAX: (617)742-7414
38     INFORMATION FOR SEQ ID NO: 16:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 553 amino acids
41     TYPE: amino acid
42     TOPOLOGY: linear
43     MOLECULE TYPE: protein
44     US-09-364-088-16

```

[illegible]





ADDRESSEE: Pillsbury Winthrop, L.L.P.  
 STREET: 1100 New York Ave., N.W.  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: MS Word

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/423,439  
 FILING DATE: 09-NOV-1999  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/GB98/01294  
 FILING DATE: 05-MAY-1998  
 APPLICATION NUMBER: GB 9709421.3

INFORMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 281 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
 US-09-423-439-44

Query Match 55.5%; Score 900.5; DB 3; Length 281;  
 Best Local Similarity 68.6%; Pred. No. 1,4e-59;  
 Matches 179; Conservative 24; Mismatches 43; Indels 15; Gaps 3;

1 MAEVKQESGGGLVOPGSGSRKLSCAASGFTFSFGHWRQAPBKLEWVAIYSSGSSSTI 60  
 21 MAEVLQESGGGLVOPGSGSRKLSCTASGFNIKQNMHWKQREQLLEWIAWIDPENGDT 80  
 61 YVADTVKGRFTISRDPKNTLFLQMTSLRSEDTVMYYC-----ARDYGVWCGT 111  
 81 EYAPKRGKATLTADSSSTAYIHLSSLSSEDTAVYCHVLIYAGYLAND--YMGQGIS 137  
 112 VTVSSGGGGSGGGSGGGSDIELTQSPAIMSAPGERVTMTCSASSSVRYNMFPQKSG 171  
 138 VAVSSGGGGSGGGSGGGSGGQILVLTQSPAIMSAPGERVTMTCSASSSVRYNMFPQKSG 197  
 172 TSPKRIYDTSKLSGVPPARFSGSGSTSYSLTSSMEADATYYCOQSSNPLTFGAG 231  
 198 TSPKMIYDTSKLSGVPPARFSGSGSTSYSLTSSMEADATYYCOQSTYPLTFGAG 257  
 232 TKLELKRRAAEOKLISEEDLN 252  
 258 TKLEIKR--EOKLISEEDLN 275

RESULT 14  
 US-09-138-091A-76  
 Sequence 76; Application US/09138091A  
 Patent No. 6737249  
 GENERAL INFORMATION:  
 APPLICANT: Adams, Camellia W.  
 APPLICANT: Carter, Paul J.  
 APPLICANT: Fendly, Brian M.  
 APPLICANT: Gurney, Austin L.  
 TITLE OF INVENTION: Agonist Antibodies  
 FILE REFERENCE: 9491-013-27  
 CURRENT APPLICATION NUMBER: US/09/138,091A  
 CURRENT FILING DATE: 1998-08-21  
 PRIOR APPLICATION NUMBER: US 60/056,736  
 PRIOR FILING DATE: 1997-08-22  
 NUMBER OF SEQ ID NOS: 77  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 76

LENGTH: 245  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: single chain antibody (scfv) fragments  
 NAME/KEY: VARIANT  
 LOCATION: 208  
 OTHER INFORMATION: Xaa = Any Amino Acid  
 US-09-138-091A-76

Query Match 55.3%; Score 897.5; DB 4; Length 245;  
 Best Local Similarity 69.8%; Pred. No. 2e-59;  
 Matches 171; Conservative 34; Mismatches 35; Indels 5; Gaps 2;

1 MAEVKQESGGGLVOPGSGSRKLSCAASGFTFSFGHWRQAPBKLEWVAIYSSGSSSTI 60  
 1 MAEVLQESGGGLVOPGSGSRKLSCTASGFNIKQNMHWKQREQLLEWIAWIDPENGDT 80  
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 117 GGGSGGGSGGGSGGGSDIELTQSPAIMSAPGERVTMTCSASSSV-RYNMFPQKSGTSPK 175  
 121 GGGSGGGSGGGSGGGSDIQMTQSPSTLASIGRVTITCRASGSIYHMLAWYQKPGKAPK 180  
 176 RMIYDTSKLSGVPPARFSGSGSTSYSLTSSMEADATYYCOQSSNPLTFGAGTKLE 235  
 181 LLIYKASLASGAPSRFSGSGSDTPTXITSSLDQDPATYYCOQSSNYPLTFGGGTKLE 240  
 236 LKRAA 240  
 241 IKRAA 245

RESULT 15  
 US-09-192-854-2  
 Sequence 2; Application US/09192854  
 Patent No. 6696245  
 GENERAL INFORMATION:  
 APPLICANT: Winter, Greg  
 APPLICANT: Tomlinson, Ian  
 TITLE OF INVENTION: Methods for selecting functional peptides  
 FILE REFERENCE: 3789/72916  
 CURRENT APPLICATION NUMBER: US/09/192,854  
 CURRENT FILING DATE: 1998-11-17  
 EARLIER APPLICATION NUMBER: 60/066,729  
 EARLIER FILING DATE: 1997-11-21  
 NUMBER OF SEQ ID NOS: 212  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 240  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-192-854-2

Query Match 55.1%; Score 894; DB 4; Length 240;  
 Best Local Similarity 71.7%; Pred. No. 3.6e-59;  
 Matches 172; Conservative 27; Mismatches 37; Indels 4; Gaps 3;

3 EYVLAQESGGGLVOPGSGSRKLSCAASGFTFSFGHWRQAPBKLEWVAIYSSGSSSTI 62  
 1 EYVLAQESGGGLVOPGSGSRKLSCTASGFNIKQNMHWKQREQLLEWIAWIDPENGDT 80  
 63 ADVKGRFTISRDPKNTLFLQMTSLRSEDTVMYYC-----YMGQGITVVS 120  
 61 ADVKGRFTISRDPKNTLFLQMTSLRSEDTVMYYC-----YMGQGITVVS 120  
 121 SGGSGGGSGGGSGGGSDIELTQSPAIMSAPGERVTMTCSASSSV-RYNMFPQKSGTSPKRI 178  
 121 SGGSGGGSGGGSGGGSDIQMTQSPSTLASIGRVTITCRASGSIYHMLAWYQKPGKAPKLI 180

Qy 179 YDTSKLSGVPAPRFGSGSGSTSYSLTISMEADATYYCOOMSSNPLTFGAGTKLELR 238  
Db 181 YAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCOOYSTPNTFGQGTKEIKR 240

Search completed: June 23, 2005, 05:55:04  
Job time : 67 secs